

Result No.	Score	Query Match Length	DB ID	Description
1	1444	100.0	268	AAB18634 Human beta1 sodium channel bet
2	789.5	55.4	272	AAB62230 Rat sodium channel bet
3	793.5	55.4	272	AAB20371 Rat beta1 subunit; Rat sodium channel
4	751	52.0	218	AAB36031 Rabbit sodium chan
5	751	52.0	218	AAB62236 Novel human diagno
6	749	51.9	218	AAB50260 Human beta3 subunit
7	263.5	18.2	1176	AAC2576 Human protein SEQ
8	258.5	17.9	159	AAB36029 Human beta3 subunit
9	258.5	17.9	22	AAB79212 Human beta3 subuni
10	258.5	17.9	21	AAB36002

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match Length	DB ID	Description
1	1444	100.0	268	AAB18634 Human beta1 sodium channel bet
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8	258.5	17.9	159	AAB36029 Human beta3 subunit
9	258.5	17.9	22	AAB79212 Human beta3 subunit
10	258.5	17.9	21	AAB36002

Title:	GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.	
Run on:	January 29, 2003, 13:24:07 ; Search time: 37 Seconds (without alignments) 965.167 Million cell updates/sec
Scoring table:	BLOSUM62
Searched:	908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters:	908470
Minimum DB seq length:	0
Maximum DB seq length:	2000000000
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	<p>A_Geneseq 101002:*</p> <p>1: /SIDS2/gcgdata/geneseq/geneseq/geneseq-emb1/AA1980.DAT:*</p> <p>2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*</p> <p>3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*</p> <p>4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*</p> <p>5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*</p> <p>6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*</p> <p>7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*</p> <p>8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*</p> <p>9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*</p> <p>10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*</p> <p>11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*</p> <p>12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*</p> <p>13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*</p> <p>14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*</p> <p>15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*</p> <p>16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*</p> <p>17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*</p> <p>18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*</p> <p>19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*</p> <p>20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*</p> <p>21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*</p> <p>22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*</p> <p>23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*</p>
RESULT 1	<p>ID AAB18634 standard; Protein: 268 AA.</p> <p>XX AAE18634;</p> <p>XX DT 17-MAY-2002 (first entry)</p> <p>XX DB Human beta1 sodium channel subunit protein.</p> <p>XX KW Human; voltage gated sodium channel; VGSC; antisense therapy; arrhythmia; gene therapy; neuropathic pain; epilepsy; anticonvulsant; analgesic; chromosome 19.</p> <p>XX OS Homo sapiens.</p> <p>XX Key Location/Qualifiers</p> <p>FT 1..16 /label= Signal_peptide</p> <p>FT 17..268 /label= Mature_beta1_sodium_channel_subunit_protein</p> <p>FT Region /note= "Hydrophobic carboxy terminal residues"</p>

PA (ORTH) ORTHO-MCNEIL PHARM INC.
 XX PI Qin N., Codd E., D'andrea M;
 XX DR WPI; 2002-17946B/23.
 DR N-PSDB; AAB29622.
 XX
 PT New human voltage gated sodium channel (VGSC) beta-1A subunit useful
 PT for identifying modulators of the functional human VGSC beta-1A
 PT subunit, for treating neuropathic or chronic pain, epilepsy, and
 arrhythmia -
 XX
 PS Claim 15; Page 96-98; 98pp; English.
 XX
 CC The invention relates to an isolated polynucleotide encoding a human
 CC voltage gated sodium channel (VGSC) beta1 subunit protein. Human beta1A
 CC sodium channel subunit protein, nucleic acids and antibodies may be used
 CC RNA or protein, and to detect and type human VGSC beta1 sodium channel
 CC subunit. Nucleotide sequences complementary to the human beta1A sodium
 CC channel subunit encoding DNA can be synthesised for antisense therapy,
 CC sodium channel subunit protein is useful for identifying modulators of
 CC channel activity or compositions comprising them are useful for treating
 CC neuropathic or chronic pain, epilepsy, and arrhythmia, which is measured
 CC by a change in sodium channel activity. VGSC beta1 subunit is useful
 CC for identifying modulators of functional human VGSC beta-1A subunit
 CC which decreases the expression of sodium channel beta1 subunit in the
 CC cells of the individual. The present sequence is human beta1A sodium
 CC channel subunit protein. Human beta1A sodium channel subunit gene is
 XX located on chromosome 19.
 SQ Sequence 268 AA;

Query Match 100 %; Score 1444; DB 23; Length 268;

Best Local Similarity 100.0%; Pred. No. 1.1e-133; Mismatches 0; Indels 0; Gaps 0;

Query 1 MGRLLALVVGALVSACGGCVCEDSETAVYGMFTKILCISKRRSETAFTTWTR 60
 Db 1 MGRLLALVVGALVSACGGCVCEDSETAVYGMFTKILCISKRRSETAFTTWTR 60

Query 61 QKGTEEFVKLRYENEVLOEEDERFEGRVMWGSRGTKDQLDSLIFTINTYNGDYE 120
 Db 61 QKGTEEFVKLRYENEVLOEEDERFEGRVMWGSRGTKDQLDSLIFTINTYNGDYE 120

Query 121 CHVYRLFFENYENTSVVKTHIEVDKGESEGACPFVTWRARWRDRWQAVRTGWL 180
 Db 121 CHVYRLFFENYENTSVVKTHIEVDKGESEGACPFVTWRARWRDRWQAVRTGWL 180

Query 181 CAMPANRPOQARAGGSSPSCPQLQWPLFSPRPGOSMPYPHRSRGYRQLCILCCWMS 240
 Db 181 CAMPANRPOQARAGGSSPSCPQLQWPLFSPRPGOSMPYPHRSRGYRQLCILCCWMS 240

Query 241 GRCLLSISQRVVLGLPGIIRCVSRGV 268
 Db 241 GRCLLSISQRVVLGLPGIIRCVSRGV 268

RESULT 2
 AAB62320
 ID AAB62320 standard; Protein; 272 AA.

AC AAB62320;
 XX DT 29-JUN-2001 (first entry)

DR Rat sodium channel beta-1A subunit.

XX Sodium channel; modulator; sodium channel beta-1A subunit; pain; rat;
 KW sodium channel alpha subunit; analgesic; neuroprotective.

OS Rattus sp.
 XX Key Location/qualifiers
 FH Misc-difference 119
 FT /note= "the corresponding nucleotide sequence encodes a
 FT residue Tyr at position 119, which is not indicated in
 FT the present sequence"
 XX PN WO200123570-A2.
 XX PD 05-APR-2001.
 XX PF 29-SEP-2000; 2000WO-US27034.
 XX PR 30-SEP-1999; 99US-0156337.
 XX PA (ORTH) ORTHO-MCNEIL PHARM INC.
 XX PI D'Andrea M, Rogers KE;
 XX DR WPI; 2001-281633/29.
 DR N-PSDB; AAF57675.
 XX PR Screening for sodium channel activity modulators, used to decrease
 PT neuropathic pain, comprises contacting a candidate compound with a cell
 PT expressing the channel -
 XX PS Example 1; Page 120-121; 124pp; English.

XX
 CC The invention relates to a method of screening for a modulator of sodium
 CC channel activity that comprises contacting a candidate modulator with a
 CC cell co-expressing a sodium channel beta1A subunit with a sodium channel
 CC alpha subunit, and determining the effect of the candidate modulator on
 CC identifying sodium channel activity in the cell. The method is useful for
 CC decreasing beta1A subunit expression. The modulators can be used to
 CC decrease neuropathic pain, and to decrease the number of febrile seizures
 CC in an individual. The present sequence represents a rat sodium channel
 XX
 SQ Sequence 272 AA;

Query Match 55.4%; Score 799.5; DB 22; Length 272;
 Best Local Similarity 68.8%; Pred. No. 5.6e-73; Mismatches 39; Indels 25; Gaps 8;

Query 1 MGRLLALVVGALVSACGGCVCEDSETAVYGMFTKILCISKRRSETAFTTWTR 60
 Db 1 MGRLLALVVGALVSACGGCVCEDSETAVYGMFTKILCISKRRSETAFTTWTR 60

Query 61 QKGTEEFVKLRYENEVLOEEDERFEGRVMWGSRGTKDQLDSLIFTINTYNGDYE 120
 Db 61 QKGTEEFVKLRYENEVLOEEDERFEGRVMWGSRGTKDQLDSLIFTINTYNGDYE 120

Query 121 CHVYRLFFENYENTSVVKTHIEVDKGESEGACPFVTWRARWRDRWQAVRTGWL 180
 Db 121 CHVYRLFFENYENTSVVKTHIEVDKGESEGACPFVTWRARWRDRWQAVRTGWL 180

Query 181 CAMPANRPOQARAGGSSPSCPQLQWPLFSPRPGOSMPYPHRSRGYRQLCILCCWMS 240
 Db 181 CAMPANRPOQARAGGSSPSCPQLQWPLFSPRPGOSMPYPHRSRGYRQLCILCCWMS 240

Query 241 GRCLLSISQRVVLGLPGIIRCVSRGV 268
 Db 241 GRCLLSISQRVVLGLPGIIRCVSRGV 268

RESULT 3
 AAB20371
 ID AAB20371 standard; Protein; 272 AA.
 XX AC AAB20371;
 XX DT 29-JUN-2001 (first entry)

DR Rat sodium channel beta-1A subunit.

XX Sodium channel; modulator; sodium channel beta-1A subunit; pain; rat;
 KW sodium channel alpha subunit; analgesic; neuroprotective.

Fri Jan 31 07:51:17 2003

DT 11-JUN-2001 (first entry)
 XX DE Sodium channel beta1A subunit.
 XX KW Sodium channel beta1A; rat; splice variant; analgesic; cardioton;
 KW pain; seizure; therapy.
 XX OS Rattus sp.
 XX
 Key Location/Qualifiers
 Peptide 1..19
 FT /label= Signal_peptide
 FT 20..272
 Protein /label= Mature_protein
 XX PT 215..233
 FT /label= Transmembrane_domain
 XX PN WO20012351-A1.
 XX PD 05-APR-2001.
 XX PP 29-SEP-2000; 2000WO-US27119.
 XX PR 30-SEP-1999; 99US-0156837.
 XX PA (UNIV MICHIGAN) ORTHO-MCNEIL PHARM INC.
 XX PI Isom LL, Kazen-Gillespie K, Rogers KE;
 XX WPI; 2001-258136/26.
 DR N-PSDB; AAF30669.
 XX An isolated nucleic acid encoding a sodium channel beta1A subunit, which is a splice variant of sodium channel beta1A polypeptide, useful for identifying modulators of sodium channel beta1A subunits and treating neuropathic pain -
 PT subunits and treating neuropathic pain -
 XX Claim 10; Page 123-124; 121pp; English.
 CC The present sequence is that of a novel rat sodium channel beta1A subunit, which is a splice variant of sodium channel beta1A resulting from retention of intron 3 containing an in-frame stop codon. This alternative splicing event produces a novel C-terminus that includes an extracellular region, a transmembrane segment, and a short intracellular domain. Western blotting showed beta1A reactive peptides of approximately 50 kDa expressed in heart, skeletal muscle, and adrenal gland, but not in adult brain or spinal cord. Methods and compositions for using beta1A proteins and nucleic acids are described. A claimed method of screening for a modulator of sodium channel activity utilises a cell co-expressing a sodium channel beta1A subunit and a sodium channel alpha subunit. A claimed method for decreasing neuropathic pain, and a claimed method for decreasing the number of fibrillar seizures in an individual, both involve administering a modulator of the sodium channel beta1A subunit.
 XX Sequence 272 AA;
 Query Match 55.4%; Score 799.5; DB 22; Length 272;
 Best Local Similarity 68.8%; Pred. No. 5..6e-73; Mismatches 14; Indels 25; Gaps 8;
 Matches 172; Conservative
 XX
 OY 1 MGRILLALWVGALVSSACGGTVEVSSETAEAVYGMTPKILCISCRSETTAETTEWFR 60
 Db 1 MGFLILALWVGAVLVSAGGCVEDSETEAVYGMTPKILCISCRSETTAETTEWFR 60
 OY 61 QKGTEBEFKVILRYENEVLOLEDEBREGGRVWNGSGTKDQDISIFTINVTNHSGDYE 120
 Db 61 QKGTEEFVKILRYENEVLOLEDEBREGGRVWNGSGTKDQDISIFTINVTNHSGDYE 119
 OY 121 CHVRLLPFENYEVNTSVKKHIEVDKGEGSGAACPTVTRARWRDWQAVDRTGWL 180
 Db 120 CHVRLLPFENYEVNTSVKKHIEVDKGNS-----LVVWQARWDRWREGDRL-- 171

OY 181 CWPANRPO--QRABEGGSSPSCPQLQWLFIFSPRPGQ-SMVPFHRSRGYRQLC---H 234
 Db 172 --VSHRGQLTTPRSRHKDTPPLVLETSAL--QHTGGQIRTPPPTING---MCIGLH 221
 OY 235 LQCMTSRCL 244
 Db 222 SCCVISBCCI 231

RESULT 4
 AAB36031
 ID AAB36031 standard; protein; 218 AA.
 XX
 AAB36031;
 AC
 XX DT 15-FEB-2001 (first entry)
 XX DE Rat beta1 subunit, SEQ ID NO: 44.
 XX Rat; beta sub-unit; beta3; analgesic; anticonvulsant;
 KW cerebroprotective; vasotropic; nootropic; cytostatic;
 KW dermatological; gene therapy; voltage-gated sodium channel; pain;
 KW epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;
 KW familial nonchromaffin paraganglioma; phenylketonuria;
 KW Charcot Marie Tooth disease; betal.
 XX OS Rattus sp.
 XX PN WO20063367-A1.
 XX PD 26-OCT-2000.
 XX PF 24-FEB-2000; 2000WO-EP01783.
 XX PR 15-APR-1999; 99US-0129473.
 XX PA (WARN) WARNER LAMBERT CO.
 PA (UCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX PI Cox P, Dixon A, Jackson A, Morgan K;
 XX DR WPI; 2000-665241/64.
 XX PT Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, useful for detecting and treating sodium channel-associated conditions, e.g. pain, epilepsy and stroke -
 PT Disclosure; Fig 4; 88pp; English.
 XX The present sequence is given in a specification relating to a novel family of beta sub-unit proteins from a voltage-gated sodium channel. Human and rat beta sub-units, which have been collectively identified as beta3, have been isolated. The polynucleotides and polypeptides are useful for screening for agonists and antagonists of sodium channels. The agonists, antagonists, proteins and nucleic acids may be used for diagnosing or treating diseases or conditions associated with voltage-gated sodium channels, e.g. pain, epilepsy, stroke, ischaemia, heart disease, Jacobsen Syndrome, Familial Nonchromaffin parangangioma, Phenylketonuria and Charcot Marie Tooth disease.
 XX SQ Sequence 218 AA;
 Query Match 52.0%; Score 751; DB 21; Length 218;
 Best Local Similarity 92.9%; Pred. No. 3..6e-68; Mismatches 9; Indels 0; Gaps 0;
 Matches 144; Conservative
 XX
 OY 1 MGRILLALWVGALVSSACGGTVEVSSETAEAVYGMTPKILCISCRSETTAETTEWFR 60
 Db 1 MGFLILALWVGAVLVSAGGCVEDSETEAVYGMTPKILCISCRSETTAETTEWFR 60
 OY 61 QKGTEEFVKILRYENEVLOLEDEBREGGRVWNGSGTKDQDISIFTINVTNHSGDYE 120
 Db 61 QKGTEEFVKILRYENEVLOLEDEBREGGRVWNGSGTKDQDISIFTINVTNHSGDYE 119
 OY 121 CHVRLLPFENYEVNTSVKKHIEVDKGEGSGAACPTVTRARWRDWQAVDRTGWL 180
 Db 120 CHVRLLPFENYEVNTSVKKHIEVDKGNS-----LVVWQARWDRWREGDRL-- 171

Db 61 QKGTEEFVKLRYNEVQLEDERFEGRVWNGSRGTRKDQLDLSIFITNVYHSGDYE 120
 Qy 121 CHVRLLFENFEHTSVVKKHLIEVVDKGESSGA 155
 Db 121 CHVRLLFENFEHTSVVKKHLIEVVDKGESSGA 155

RESULT 5
 AAB62326
 ID AAB62326 standard; Protein; 218 AA.
 AC AAB62326;
 DT 29-JUN-2001 (first entry)
 DE Rat sodium channel beta-1 subunit amino acid sequence.
 XX
 KW sodium channel; modulator; sodium channel beta-1A subunit; pain; rat;
 XX
 KW sodium channel beta-1 subunit; analgesic; neuroprotective.
 OS Rattus sp.
 PN WO200123570-A2.
 PD 05-APR-2001.
 XX
 PP 29-SEP-2000; 2000WO-US27034.
 XX
 PR 30-SEP-1999; 99US-0156337.
 XX
 PA (ORTH) ORTHO-MCNEIL PHARM INC.
 PT XX
 PI D'Andrea M, Rogers KE;
 DR XX
 DR WPI; 2001-281683/29.

PT screening for sodium channel activity modulators, used to decrease neuropathic pain, comprises contacting a candidate compound with a cell expressing the channel - Examples; Fig 1B; 124pp; English.

CC The invention relates to a method of screening for a modulator of sodium channel activity that comprises contacting a candidate modulator with a cell co-expressing a sodium channel beta-1A subunit with a sodium channel alpha subunit, and determining the effect of the candidate modulator on the sodium channel function in the cell. The method is useful for identifying sodium channel activity modulators, preferably causing decreased neuropathic pain, and to decrease the number of fibrile seizures in an individual. The present sequence represents a rat sodium channel beta-1 subunit, used in homology studies with the beta-1A subunit.

SQ Sequence 218 AA;

Query Match Best Local Similarity Score 749; DB 22; Length 218;
 Matches 144; Conservative 92.9%; Pred. No. 5.8e-68; Mismatches 9; Indels 0; Gaps 0;

Db 1 MGRLLALVVGALVSSACGGCVDSETAEAVGMFKLICISCRRSSTAETPTTETFR 60
 1 MGRLLALVVGALVSSACGGCVDSETAEAVGMFKLICISCRRSSTAETPTTETFR 60

Qy 61 QKGTEEFVKLRYNEVQLEDERFEGRVWNGSRGTRKDQLDLSIFITNVYHSGDYE 120
 Db 61 QKGTEEFVKLRYNEVQLEDERFEGRVWNGSRGTRKDQLDLSIFITNVYHSGDYE 120
 1 MGRLLALVVGALVSSACGGCVDSETAEAVGMFKLICISCRRSSTAETPTTETFR 60

Qy 61 QKGTEEFVKLRYNEVQLEDERFEGRVWNGSRGTRKDQLDLSIFITNVYHSGDYE 120
 Db 61 QKGTEEFVKLRYNEVQLEDERFEGRVWNGSRGTRKDQLDLSIFITNVYHSGDYE 120
 1 MGRLLALVVGALVSSACGGCVDSETAEAVGMFKLICISCRRSSTAETPTTETFR 60

Qy 61 QKGTEEFVKLRYNEVQLEDERFEGRVWNGSRGTRKDQLDLSIFITNVYHSGDYE 120
 Db 61 QKGTEEFVKLRYNEVQLEDERFEGRVWNGSRGTRKDQLDLSIFITNVYHSGDYE 120
 1 MGRLLALVVGALVSSACGGCVDSETAEAVGMFKLICISCRRSSTAETPTTETFR 60

Qy 121 CHVRLLFENFEHTSVVKKHLIEVVDKGESSGA 155
 Db 121 CHVRLLFENFEHTSVVKKHLIEVVDKGESSGA 155

RESULT 6
 AAB62326
 ID AAB62326 standard; Protein; 218 AA.
 AC AAB62326;
 DT 13-MAR-2001 (first entry)
 DE Rabbit sodium channel beta1 protein.
 XX
 KW Rat; sodium channel beta3 protein; Altxa94h5; pain; sleep disorder; neurodegenerative disorder; mood disorder; muscle contraction.
 XX
 OS Oryctolagus cuniculus.
 PN WO200069912-A1.
 PD 23-NOV-2000.
 XX
 PP 12-MAY-2000; 2000WO-US13144.
 XX
 PR 14-MAY-1999; 99US-0134198.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PT XX
 PI Curtis RAJ;
 XX
 DR WPI; 2001-122743/13.

PT New rat sodium channel beta-3 subunit gene isolated from a rat dorsal root ganglion cDNA library for use in chromosome mapping, forensic medicine, monitoring clinical trials and therapeutics - Disclosure; Fig 3; 145pp; English.

CC The present invention provides the protein and coding sequences of the rat sodium channel beta3 protein, designated Altxa94h5. This protein is involved in the generation of pain and other sensory or perceptive nerve impulses, in the establishment and endurance of mood, neurodegenerative and sleep disorders, and in the control of muscle contraction, including movements such as the heartbeat, digestion and vascular tone. The sequences can be used in predictive medicine, screening and diagnostic assays, and in pharmacogenomics.

CC Sequence 218 AA;

Query Match Best Local Similarity Score 749; DB 22; Length 218;
 Matches 144; Conservative 92.9%; Pred. No. 5.8e-68; Mismatches 9; Indels 0; Gaps 0;

Db 1 MGRLLALVVGALVSSACGGCVDSETAEAVGMFKLICISCRRSSTAETPTTETFR 60
 1 MGRLLALVVGALVSSACGGCVDSETAEAVGMFKLICISCRRSSTAETPTTETFR 60

Qy 61 QKGTEEFVKLRYNEVQLEDERFEGRVWNGSRGTRKDQLDLSIFITNVYHSGDYE 120
 Db 61 QKGTEEFVKLRYNEVQLEDERFEGRVWNGSRGTRKDQLDLSIFITNVYHSGDYE 120
 1 MGRLLALVVGALVSSACGGCVDSETAEAVGMFKLICISCRRSSTAETPTTETFR 60

Qy 121 CHVRLLFENFEHTSVVKKHLIEVVDKGESSGA 155
 Db 121 CHVRLLFENFEHTSVVKKHLIEVVDKGESSGA 155

RESULT 7
 ABG22576
 ID ABG22576 standard; Protein; 1176 AA.
 XX
 AC ABG22576;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #22567.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensics;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PR 31-MAR-2001; 2001WO-US08631.

XX

PR 23-AUG-2000; 2000US-0649167.

XX

PA (NYSE-) NYSEQ INC.

XX

PT Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

XX

PT New isolated Polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -

XX

PS N-PSDB; AAS86763.

XX

CC The invention relates to isolated Polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG3377 represent novel human

CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at http://www.wipo.int/pct/published_pct_sequences.

XX

SQ Sequence 1176 AA;

XX

Query Match 18.2%; Score 263.5; DB 22; Length 1176;

Best Local Similarity 41.6%; Pred. No. 1.7e-17;

Matches 62; Conservative 20; Mismatches 54; Indels 13; Gaps 5;

XX

Oy 21 CVEDSETAEVYGMKTKLCTSKCRSERSETAETIEWTFRQKGTEFVKILRYENEVLQL 80

Db 994 CVEVPSETEAVYOGNPMKLRCLSCMKREVEATTVWFRPECGKDFL-IYBVRNGHOEV 1052

Oy 81 EEDEREGRGRVWNGSGRTKDLQDLSIFITNTVYHNSGDECHVYRFLPENYHNTSVK 140

Db 1053 ESP--FQGRQLQWNS--KDLQDPSVTIVLNLTANDSGLYTCNVNSREFEFAHRPFVKTR 1107

Oy 141 KTHIEVDKG--ESGACAPFTV---TH 162

Db 1108 LIFPLRVTEGLLISNNVNPMLIELGRNTH 1136

XX

SQ Sequence 159 AA;

XX

Query Match 17.9%; Score 258.5; DB 21; Length 159;

Best Local Similarity 43.2%; Pred. No. 3.7e-18;

Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

XX

Oy 5 LALVGAALVSAGSGCTVEDSETAEVYGMKTKLCTSKCRSERSETAETIEWTFRQKG 64

Db 10 LASLVLIVYWSVCPPVCPVSEPSITEAVYOGNPMKLRCLSCMKREVEATTVWFRPEG 69

Oy 65 BEFKILRYENEVLQLEEDEREGRGRVWNGSGRTKDLQDLSIFITNTVYHNSGDECHV 124

Db 70 KDFL-IYBVRNGHOEVES--FQGRQLQNS--KDLQDPSVTIVLNLTANDSGLYTCNV 123

Oy 125 RLLFFENYHNTSVKHKIEVDKG--ESGACAPFTV---TH 151

Db 124 REPERFAHRPFVKTRLIPRLPVTEAGE 151

XX

RESULT 9

AAM79212

ID AAM79212 Standard; Protein: 195 AA.

XX

AC AAM79212;

XX

RESULT 8
ID AAB36020
XX AAB36020 standard; protein: 159 AA.
AC AAB36020;

DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 1874.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haemopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 OS Homo sapiens.
 XX
 PN WO20015190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PR 05-FEB-2001; 2001WO-US04098.
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX
 PA (HYSE-) HYSQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 XX
 PI Xue AJ, Yang Y, Wejhran T, Goodrich R;
 DR WPI; 2001-476283/51.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 PS Claim 20; Page 4260; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAKS1456-AAKS3435) and the
 CC encoded polypeptides (AAW8322-AAW0302) that exhibit activity relating to
 CC production of other cytokines or cell differentiation or which may induce
 CC poly nucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 e.g. stem cell growth factor activity, haemopoiesis regulating
 activity, tissue growth factor activity, immunomodulatory activity and
 activin/inhibin activity and may be useful in the diagnosis and/or
 treatment of cancer, leukaemia, nervous system disorders, arthritis and
 inflammation.
 Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 (AAW0020) are omitted as the relevant pages from the sequence listing
 were missing at the time of publication.

SQ Sequence 195 AA;

Query Match 17.9%; Score 258.5; DB 22; length 195;
 Best Local Similarity 43.2%; Pred. No. 4.9e-18;
 Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

QY 5 LALVYGAALVSSACGGCVERDSETEAVGWTFLKLICISKRSSETNAETFTWTFRKGT 64
 10 LASLVLIVYWVSVCPVCVCEVPSETEAVQGNPMKURCISCMKREBEAVTIVVWFPYRPEGG 69

QY 65 BEFPFKILRYENEVQLLEDERFERFGRVWNGSGRTKDQLDSLSTFINVWVNHGDYEHVY 124

DB 70 KDFL-IYEYRNHGHOEVSP--FOGLQWNGS--KDLQDVSIWLNVLTNDSGLYCNVS 123

QY 125 RLFFENYENNTSVKKHIEVVDK-GE 151

DB 124 REFFEEAHRRPFVKTRPLRVMEAGE 151

SQ Sequence 215 AA;

Query Match 17.9%; Score 258.5; DB 21; length 215;
 Best Local Similarity 43.2%; Pred. No. 5.6e-18;
 Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

QY 5 LALVYGAALVSSACGGCVERDSETEAVGWTFLKLICISKRSSETNAETFTWTFRKGT 64
 10 LASLVLIVYWVSVCPVCVCEVPSETEAVQGNPMKURCISCMKREBEAVTIVVWFPYRPEGG 69

QY 65 BEFPFKILRYENEVQLLEDERFERFGRVWNGSGRTKDQLDSLSTFINVWVNHGDYEHVY 124

DB 70 KDFL-IYEYRNHGHOEVSP--FOGLQWNGS--KDLQDVSIWLNVLTNDSGLYCNVS 123

QY 125 RLFFENYENNTSVKKHIEVVDK-GE 151

DB 124 REFFEEAHRRPFVKTRPLRVMEAGE 151

RESULT 11
 AAB85206 standard; Protein; 215 AA.
 ID AAB85206;
 AC XX
 XX 07-SEP-2001 (first entry)
 DE Human novel sodium channel betal-like subunit.
 KW Sodium channel; sensory neurone specific channel; betal-like subunit;
 SNS; therapeutic; pain; analgesic.
 XX OS Homo sapiens.
 FH XX
 FT Key Location/Qualifiers
 Domain 38 .122 /note= "immunoglobulin domain"
 FT 157 .176 /note= "transmembrane domain"
 FT XX
 PN WO200144293-A2.
 PD XX
 XX 21-JUN-2001.
 PT XX
 PR 14-DEC-2000; 2000WO-GB04802.
 PT XX
 PR 17-DEC-1999; 99GB-0029970.
 PA XX
 PA (GLAXO) GLAXO GROUP LTD.
 PT XX
 PT Plumpton M, Powell AJ, Sanseau P;
 XX WPI; 2001-398129/42.
 DR XX
 DR N-PSDB; AAF84146.
 PA XX
 PA Novel sub-unit for voltage-gated sodium channel proteins for producing
 agents useful for treating pain
 XX
 PS Claim 1; Fig 2; 31pp; English.
 CC XX
 CC The invention provides a novel betal-like sub-unit for voltage-gated
 sodium ion channel polypeptide, specifically a sensory neurone specific
 channel (SNS) subunit. The novel betal-like subunit is useful for
 producing a therapeutic agent which is useful treating pain in a patient.
 CC The subunit can be expressed by standard recombinant methodology. The
 present sequence represents a human novel sodium channel betal-like
 subunit.
 CC XX
 CC Sequence 215 AA;
 CC The invention provides a novel betal-like sub-unit for voltage-gated
 sodium ion channel polypeptide, specifically a sensory neurone specific
 channel (SNS) subunit. The novel betal-like subunit is useful for
 producing a therapeutic agent which is useful treating pain in a patient.
 CC The subunit can be expressed by standard recombinant methodology. The
 present sequence represents a human novel sodium channel betal-like
 subunit.
 SQ XX
 SQ The present invention describes assemblages and computer readable media
 comprising novel human cDNA sequences and clones derived from human
 foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
 libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
 present invention which encode the proteins given in ABB0562 to
 CC ABB05729. The human cDNA sequences and clones can be used in gene
 therapy. The clones may be used in a variety of applications, for
 example they may be used in profiling assays, for providing large arrays
 CC of human genetic material for implementing large-scale screening
 CC strategies and for treating diseases via gene therapy procedures.
 SQ XX
 SQ Sequence 215 AA;
 SQ The present invention describes assemblages and computer readable media
 comprising novel human cDNA sequences and clones derived from human
 foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
 libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
 present invention which encode the proteins given in ABB0562 to
 CC ABB05729. The human cDNA sequences and clones can be used in gene
 therapy. The clones may be used in a variety of applications, for
 example they may be used in profiling assays, for providing large arrays
 CC of human genetic material for implementing large-scale screening
 CC strategies and for treating diseases via gene therapy procedures.
 SQ XX
 SQ Best Local Similarity 17.9%; Score 258.5; DB 22; Length 215;
 Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;
 Best Local Similarity 43.2%; Pred. No. 5.6e-18;
 Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;
 Best Local Similarity 43.2%; Pred. No. 5.6e-18;
 Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;
 Qy 5 LALVVGALVSSACCGCVEUDSETEAVYQNTFKILCISCKRASSETNAETFIEWTFRQGT 64
 Db 10 LASLVLIVWVSCFPVCVEVSETEAVQCNPMKLCISCKMREVEATTVVVFYRPEGG 69
 Qy 65 EEFVKILRYENEVQLQEBDERPREGVWNGSRSRJTKDQLSTFINTVNHAGGYCHY 124
 Db 70 KDFL-IIVYRNGHQEVSP-FOGRLOWNGS---KDLQDVSVITLVNLNTDSLGYTCNVS 123
 Qy 125 RLLPFENYERHTSVVKKIHIEVDK-GE 151
 Db 124 REFEFAHRPPVKTRLIPLRVTEAGE 151
 RESULT 13
 AAB36021 standard; protein; 159 AA.
 ID AAB36021
 XX 15-FEB-2001 (first entry)
 DE XX
 Rat beta3 subunit peptide, SEQ ID NO: 23.
 KW XX
 Rat; beta sub-unit; bet3; analgesic; anticonvulsant;

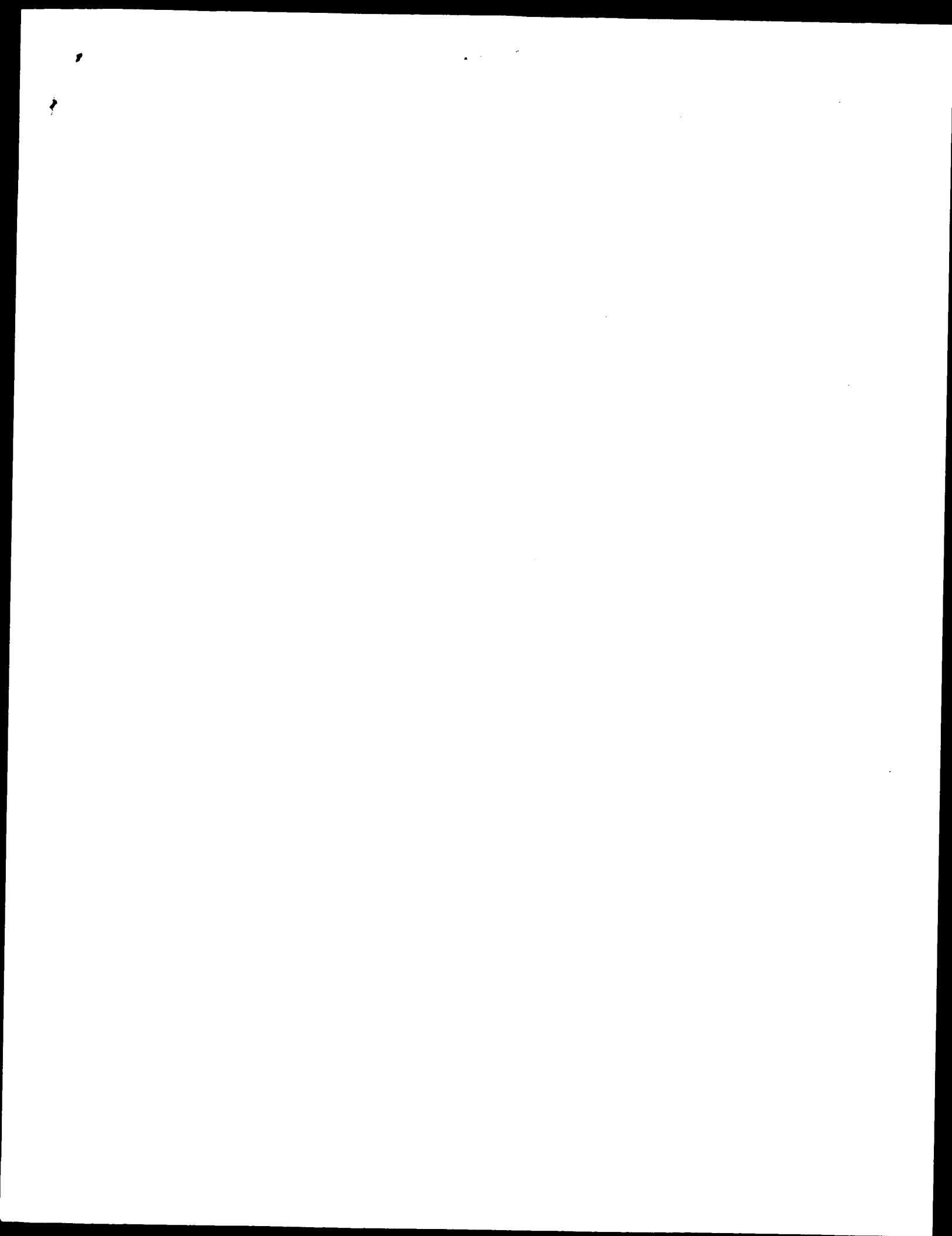
RESULT 12
 AAB05689 standard; Protein; 215 AA.
 ID AAB05689

KW cerebroprotective; vasotropic; cardiotropic; nootropic; cytostatic;
 KW dermatological; gene therapy; voltage-gated sodium channel; pain;
 KW epilepsy; stroke; ischaemia; heart disease; Jacobsen Syndrome;
 KW Charcot Marie Tooth disease.
 XX OS Rattus sp.
 XX XX OS Rattus sp.
 XX PN WO200063367-A1.
 XX PD 12-MAY-2000; 2000WO-US13144.
 XX 26-OCT-2000.
 XX PR 14-MAY-1999; 99US-0134198.
 XX PF 24-FEB-2000; 2000WO-EP01783.
 XX PR 15-APR-1999; 99US-0129473.
 XX PA (WARN) WARNER LAMBERT CO.
 PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 PA XX Cox P., Dixon A., Jackson A., Morgan K.;
 PT DR WPI; 2000-655241/64.
 PR XX Novel nucleic acids encoding a beta-3 subunit from a voltage-gated
 PT sodium channel, and their corresponding polypeptides, useful for
 PT detecting and treating sodium channel-associated conditions, e.g. pain,
 PR XX epilepsy and stroke -
 PS Claim 36; Page 76-77; 88pp; English.
 CC The present sequence is given in the claims of a specification
 CC relating to a novel family of beta sub-unit proteins from a
 CC voltage-gated sodium channel. Human and rat beta sub-units, which
 CC have been collectively identified as beta3, have been isolated.
 CC The polynucleotides and polypeptides are useful for screening for
 CC agonists and antagonists of sodium channels. The agonists, antagonists,
 CC proteins and nucleic acids may be used diagnosing or treating diseases
 CC or conditions associated with voltage-gated sodium channels, e.g. pain,
 CC epilepsy, stroke, ischaemia, heart disease, Jacobsen Syndrome, Familial
 CC Nonchromaffin Paraganglioma, Phenylketonuria and Charcot Marie Tooth
 XX disease.
 SQ Sequence 159 AA;
 Query Match Best Local Similarity 17.8%; Score 257.5; DB 21; Length 159;
 Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;
 QY OY 21 CVEDSETEAIVGMKILCISCKRSRSETNAETTEWTFRQKGTFKILRYENEVQL 80
 Db 26 CVEVPSETEAIVGMPKLRCSOMKREVEATVWVYFPRPEGKDFL-IYEYRNHOEV 84
 QY 81 EEDERFGRGVWNGSRGKTDIQLDISIFITNTVYHSGYECHYRLPFENNTNISVWK 140
 Db 85 ESP--FOGRQWGS--KDLQDVSIIVNLNDGLYTGNVAREFEBAHRPFVKTR 139
 QY 141 KHIIEVVDK-GE 151
 Db 140 LIPLRVTEAGE 151
 RESULT 14
 AAB50245 ID AAB50245 standard; Protein; 191 AA.
 XX AC AAB50245;
 XX DT 13-MAR-2001 (first entry)
 XX DE Rat beta3 subunit.
 XX Rat; beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;
 KW vasotropic; cardiotropic; nootropic; cytostatic; dermatological;
 KW gene therapy; voltage-gated sodium channel; pain; epilepsy; stroke;
 KW ischaemia; heart disease; Jacobsen Syndrome;
 KW familial nonchromaffin paraganglioma; phenylketonuria;
 KW Charcot Marie Tooth disease.
 XX OS Rattus sp.
 XX PN WO200063367-A1.

PD 26-OCT-2000.
 XX
 PF 24-FEB-2000; 2000W0-EPO1783.
 XX
 PR 15-APR-1999; 99US-0129473.
 XX
 PA (WARN) WARNER LAMBERT CO.
 PA (UTCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
 XX
 PI Cox P, Dixon A, Jackson A, Morgan K;
 XX DR WPI; 2000-665241/64.
 XX DR N-PSDB; AAC67836.
 PT Novel nucleic acids encoding a beta-3 subunit from a voltage-gated
 PT Sodium channel, and their corresponding polypeptides useful for
 PT detecting and treating sodium channel-associated conditions, e.g. pain,
 PT epilepsy and stroke -
 XX
 PS Claim 33; Fig 4; 88pp; English.
 XX
 CC The present sequence is given in the claims of a specification
 CC relating to a novel family of beta sub-unit proteins from a
 CC voltage-gated sodium channel. Human and rat beta sub-units, which
 CC have been collectively identified as beta3, have been isolated.
 CC The polynucleotides and polypeptides are useful for screening for
 CC agonists and antagonists of sodium channels. The agonists, antagonists,
 CC proteins and nucleic acids may be used diagnosing or treating diseases
 CC or conditions associated with voltage-gated sodium channels, e.g. pain,
 CC epilepsy, stroke, ischaemia, heart disease, Jacobsen Syndrome, Familial
 CC Nonchromaffin Paranganglioma, Phenylketonuria and Charcot Marie Tooth
 CC disease.
 XX
 SQ Sequence 215 AA;

Query Match 17.8%; Score 257.5; DB 21; Length 215;
 Best Local Similarity 44.7%; Pred. No. 7e-18; Gaps 4;
 Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;
 Local Similarity 44.7%; Pred. No. 7e-18; Gaps 4;
 Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;
 OY 21 CYPFDSETEAVVGMTPKILCISCKRSETNAEKFIEWTFEROKGKPFVKILVENEVQL 80
 Db 26 CYPVPSETEAQGNPKLRCISOMKREBEATVVEWFPPEGSKDFL-TYEYANGHQBV 84
 Qy 81 EEPERFGRVUUNGSRGTRKDQLSITPNTVNNISGDYCHVVRLFFENYENTSVK 140
 Db 85 ESS--FOGLONGS--KDLOPVSTVLNLINDSGLYCNNSREFEEAHRFVKTR 139
 Qy 141 KHEVDK-GE 151
 Db 140 LIPLRVTEAGE 151

Search completed: January 29, 2003, 13:28:15
 Job time : 38 secs



; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-430-503-24

Query Match 8.0%; Score 115.5; DB 4; Length 209;
Best Local Similarity 30.6%; Pred. No. 0.00019; Matches 38; Conservative 17; Mismatches 62; Indels 7; Gaps 4;
Matches 38; Conservative 17; Mismatches 62; Indels 7; Gaps 4;
QY 3 RLLALVVGAL-VSSACGGCVEDSETE--AVYGMTPKILCISCKRSETNAETFWTF 59
Db 18 RMLWSVLAALGILTAGSALEYVTPEKFVANGTOKLTC-KFKSTSTGGITSVWSWP 76
QY 60 RQKGTEEFVKILRYENEVQLQLEDERFGRGVWNGSRGKTDQDLSIFITNTYHSGDY 119
Db 77 QPEGADTTVSFFHYSQGQVLYGNYPFPFKDRISW--AGDLKKDASINIENMQPHNGTY 133
QY 120 ECHV 123
Db 134 ICDV 137

RESULT 3
US-09-430-503-4

; Sequence 4, Application US/09430503
; Patent No. 6355786

GENERAL INFORMATION:

APPLICANT: Zhao, Zhi-zhuang

TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND THERAPEUTIC AND SCREENING METHODS USING SAME

FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2

CURRENT APPLICATION NUMBER: US/09/430,503

CURRENT FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 269

TYPE: PRT
ORGANISM: Homo sapiens

RESULT 3
US-09-430-503-4

; Query Match 8.0%; Score 115.5; DB 4; Length 269;
Best Local Similarity 30.6%; Pred. No. 0.00027; Matches 38; Conservative 17; Mismatches 62; Indels 7; Gaps 4;

Matches 38; Conservative 17; Mismatches 62; Indels 7; Gaps 4;

QY 3 RLLALVVGAL-VSSACGGCVEDSETE--AVYGMTPKILCISCKRSETNAETFWTF 59

Db 18 RMLWSVLAALGILTAGSALEYVTPEKFVANGTOKLTC-KFKSTSTGGITSVWSWP 76

QY 60 RQKGTEEFVKILRYENEVQLQLEDERFGRGVWNGSRGKTDQDLSIFITNTYHSGDY 119

Db 77 QPEGADTTVSFFHYSQGQVLYGNYPFPFKDRISW--AGDLKKDASINIENMQPHNGTY 133

QY 120 ECHV 123

Db 134 ICDV 137

RESULT 5
US-09-430-503-8

; Sequence 8, Application US/09430503
; Patent No. 6355786

GENERAL INFORMATION:

APPLICANT: Zhao, Zhi-zhuang

TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND THERAPEUTIC AND SCREENING METHODS USING SAME

FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2

CURRENT APPLICATION NUMBER: US/09/430,503

CURRENT FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 269

TYPE: PRT
ORGANISM: Homo sapiens

RESULT 5
US-09-430-503-8

; Query Match 8.0%; Score 115.5; DB 4; Length 269;
Best Local Similarity 30.6%; Pred. No. 0.00027; Matches 38; Conservative 17; Mismatches 62; Indels 7; Gaps 4;

Matches 38; Conservative 17; Mismatches 62; Indels 7; Gaps 4;

QY 3 RLLALVVGAL-VSSACGGCVEDSETE--AVYGMTPKILCISCKRSETNAETFWTF 59

Db 18 RMLWSVLAALGILTAGSALEYVTPEKFVANGTOKLTC-KFKSTSTGGITSVWSWP 76

QY 60 RQKGTEEFVKILRYENEVQLQLEDERFGRGVWNGSRGKTDQDLSIFITNTYHSGDY 119

Db 77 QPEGADTTVSFFHYSQGQVLYGNYPFPFKDRISW--AGDLKKDASINIENMQPHNGTY 133

QY 120 ECHV 123

Db 134 ICDV 137

RESULT 6
US-09-430-503-34

; Sequence 34, Application US/09430503
; Patent No. 6355786

GENERAL INFORMATION:

APPLICANT: Zhao, Zhi-zhuang

TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND THERAPEUTIC AND SCREENING METHODS USING SAME

FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2

CURRENT APPLICATION NUMBER: US/09/430,503

CURRENT FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 34

LENGTH: 159

RESULT 3
US-09-430-503-6

; Sequence 6, Application US/09430503
; Patent No. 6355786

GENERAL INFORMATION:

APPLICANT: Zhao, Zhi-zhuang

TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND THERAPEUTIC AND SCREENING METHODS USING SAME

FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2

CURRENT APPLICATION NUMBER: US/09/430,503

CURRENT FILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 49

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

LENGTH: 269

; ORGANISM: Homo sapiens
; US-09-430-503-34

Query Match 7.9%; Score 114.5; DB 4; Length 159;
Best Local Similarity 30.6%; Pred. No. 0.00022; Length 159;
Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;
Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;
Patent No. 6355786

QY 3 RILALVVGALVSSACG-GCDEVSETE-AVYGMFKILCISCKRSETNAETTEWTF 59
Db 18 RWLWSVLAALGLITAGVSALLEVTPKEIFVANGTQKULC-KFKSTSTGGLTSVWSF 76

QY 60 ROKTTEBFVKLRYENEVLOQEDERFGRVWNGSGTKDQLDISITINTVNHSGY 119
Db 77 QPEGADTVSFFHYSQGVYLGNYPFPFKDRISW--AGDLDDKKDASINENMQFIHNGTY 133

QY 120 ECHV 123
Db 134 ICDV 137

US-09-430-503-42

Query Match 7.9%; Score 114.5; DB 4; Length 199;
Best Local Similarity 30.6%; Pred. No. 0.00022; Length 199;
Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;
Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;
Patent No. 6355786

QY 3 RILALVVGALVSSACG-GCDEVSETE-AVYGMFKILCISCKRSETNAETTEWTF 59
Db 18 RWLWSVLAALGLITAGVSALLEVTPKEIFVANGTQKULC-KFKSTSTGGLTSVWSF 76

QY 60 ROKTTEBFVKLRYENEVLOQEDERFGRVWNGSGTKDQLDISITINTVNHSGY 119
Db 77 QPEGADTVSFFHYSQGVYLGNYPFPFKDRISW--AGDLDDKKDASINENMQFIHNGTY 133

QY 120 ECHV 123
Db 134 ICDV 137

RESULT 9

US-09-430-503-46
; Sequence 46, Application US/09430503

; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhihuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 38
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-430-503-46
Query Match 7.9%; Score 114.5; DB 4; Length 199;
Best Local Similarity 30.6%; Pred. No. 0.00022; Length 199;
Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;
Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;
Patent No. 6355786

QY 3 RILALVVGALVSSACG-GCDEVSETE-AVYGMFKILCISCKRSETNAETTEWTF 59
Db 18 RWLWSVLAALGLITAGVSALLEVTPKEIFVANGTQKULC-KFKSTSTGGLTSVWSF 76

QY 60 ROKTTEBFVKLRYENEVLOQEDERFGRVWNGSGTKDQLDISITINTVNHSGY 119
Db 77 QPEGADTVSFFHYSQGVYLGNYPFPFKDRISW--AGDLDDKKDASINENMQFIHNGTY 133

QY 120 ECHV 123
Db 134 ICDV 137

RESULT 8

US-09-430-503-42
; Sequence 42, Application US/09430503
; Patent No. 6355786

; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhihuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 42
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 10

US-09-430-503-18
; Sequence 18, Application US/09430503
; Patent No. 6355786

; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhihuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 18
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-430-503-18

Query Match 7.9%; Score 114.5; DB 4; Length 209;
 Best Local Similarity 30.6%; Pred. No. 0.00024;
 Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;

Qy 3 RLLALVVGALVSSACG-GCVERUDSETE-AVYGMTPKILCISCRSERSETNAEPTFWTF 59
 Db 18 RWLWSVLAALGILTAGVSALLEVYTPKEIFVANGTQGKLTIC-KFKSTSTGGLTSVWSF 76

Qy 60 ROKGTEREFVKILRVEENVOLLEDERPREGRVWNGSRGTQKLDLSIFTNVNTHSGDY 119
 Db 77 QPEGADTTVSFFHYSQGVIGNYPFPKDRISW--AGDLDKDASINENMQFLHNGTY 133

Qy 120 ECHV 123
 Db 134 ICDV 137

RESULT 11
 US-09-430-503-22
 ; Sequence 22, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhao, Zhihuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 22
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-430-503-22

Query Match 7.9%; Score 114.5; DB 4; Length 209;
 Best Local Similarity 30.6%; Pred. No. 0.00024; Mismatches 64; Indels 7; Gaps 4;

Qy 3 RLLALVVGALVSSACG-GCVERUDSETE-AVYGMTPKILCISCRSERSETNAEPTFWTF 59
 Db 18 RWLWSVLAALGILTAGVSALLEVYTPKEIFVANGTQGKLTIC-KFKSTSTGGLTSVWSF 76

Qy 60 ROKGTEREFVKILRVEENVOLLEDERPREGRVWNGSRGTQKLDLSIFTNVNTHSGDY 119
 Db 77 QPEGADTTVSFFHYSQGVIGNYPFPKDRISW--AGDLDKDASINENMQFLHNGTY 133

Qy 120 ECHV 123
 Db 134 ICDV 137

RESULT 12
 US-09-430-503-2
 ; Sequence 2, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhao, Zhihuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 2
 ; LENGTH: 209
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-430-503-2

Query Match 7.9%; Score 114.5; DB 4; Length 209;
 Best Local Similarity 30.6%; Pred. No. 0.00024; Mismatches 64; Indels 7; Gaps 4;

Qy 3 RLLALVVGALVSSACG-GCVERUDSETE-AVYGMTPKILCISCRSERSETNAEPTFWTF 59
 Db 18 RWLWSVLAALGILTAGVSALLEVYTPKEIFVANGTQGKLTIC-KFKSTSTGGLTSVWSF 76

Qy 60 ROKGTEREFVKILRVEENVOLLEDERPREGRVWNGSRGTQKLDLSIFTNVNTHSGDY 119
 Db 77 QPEGADTTVSFFHYSQGVIGNYPFPKDRISW--AGDLDKDASINENMQFLHNGTY 133

Qy 120 ECHV 123
 Db 134 ICDV 137

RESULT 13
 US-09-430-503-36
 ; Sequence 36, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhao, Zhihuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 36
 ; LENGTH: 159
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-430-503-36

Query Match 7.8%; Score 112.5; DB 4; Length 159;
 Best Local Similarity 29.8%; Pred. No. 0.00027; Mismatches 64; Indels 7; Gaps 4;

Qy 3 RLLALVVGALVSSACG-GCVERUDSETE-AVYGMTPKILCISCRSERSETNAEPTFWTF 59
 Db 18 RWLWSVLAALGILTAGVSALLEVYTPKEIFVANGTQGKLTIC-KFKSTSTGGLTSVWSF 76

Qy 60 ROKGTEREFVKILRVEENVOLLEDERPREGRVWNGSRGTQKLDLSIFTNVNTHSGDY 119
 Db 77 QPEGADTTVSFFHYSQGVIGNYPFPKDRISW--AGDLDKDASINENMQFLHNGTY 133

Qy 120 ECHV 123
 Db 134 ICDV 137

RESULT 14
 US-09-430-503-40
 ; Sequence 40, Application US/09430503
 ; Patent No. 6355786
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhao, Zhihuang
 ; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND FILE REFERENCE: ATTORNEY DOCKET NO. 6355786 1242-11/2
 ; CURRENT APPLICATION NUMBER: US/09/430,503
 ; CURRENT FILING DATE: 1999-10-29
 ; NUMBER OF SEQ ID NOS: 49
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 40
 ; LENGTH: 159
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-430-503-40

Query Match 7.8%; Score 112.5; DB 4; Length 159;

Best Local Similarity 29.8%; Pred. No. 0.00027; Matches 37; Conservative 16; Mismatches 64; Indels 7; Gaps 4;

Qy 3 RLLALVVGALVSSACG-GCVERDSETE-AVYGMTPKILCISCKERSENAETFWRP 59
Db 18 RLLALVGLAATGILTAGVSALLEVYTPKEIFVANGTQKLTC-KPKSTSTRGGLTSVWSF 76

Qy 60 ROKGTEEFVKILRYENEVLOLEEDERFEGRVVWMSRGTKDLSIFTINVTNHSGDY 119
Db 77 QPEGADITVSPPHYSQQVYIGNPPFKDRSW--AGDLDKDASINMNOFHNGTY 133

Qy 120 ECHV 123
Db 134 ICDV 137

RESULT 15
US-09-430-503-44
; Sequence 44 Application US/09430503
; Patent No. 6355786
; GENERAL INFORMATION:
; APPLICANT: Zhao, Zhi-zhuang
; TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. 6355786 1242-11/2
; CURRENT APPLICATION NUMBER: US/09/430,503
; CURRENT FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 44
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-430-503-44

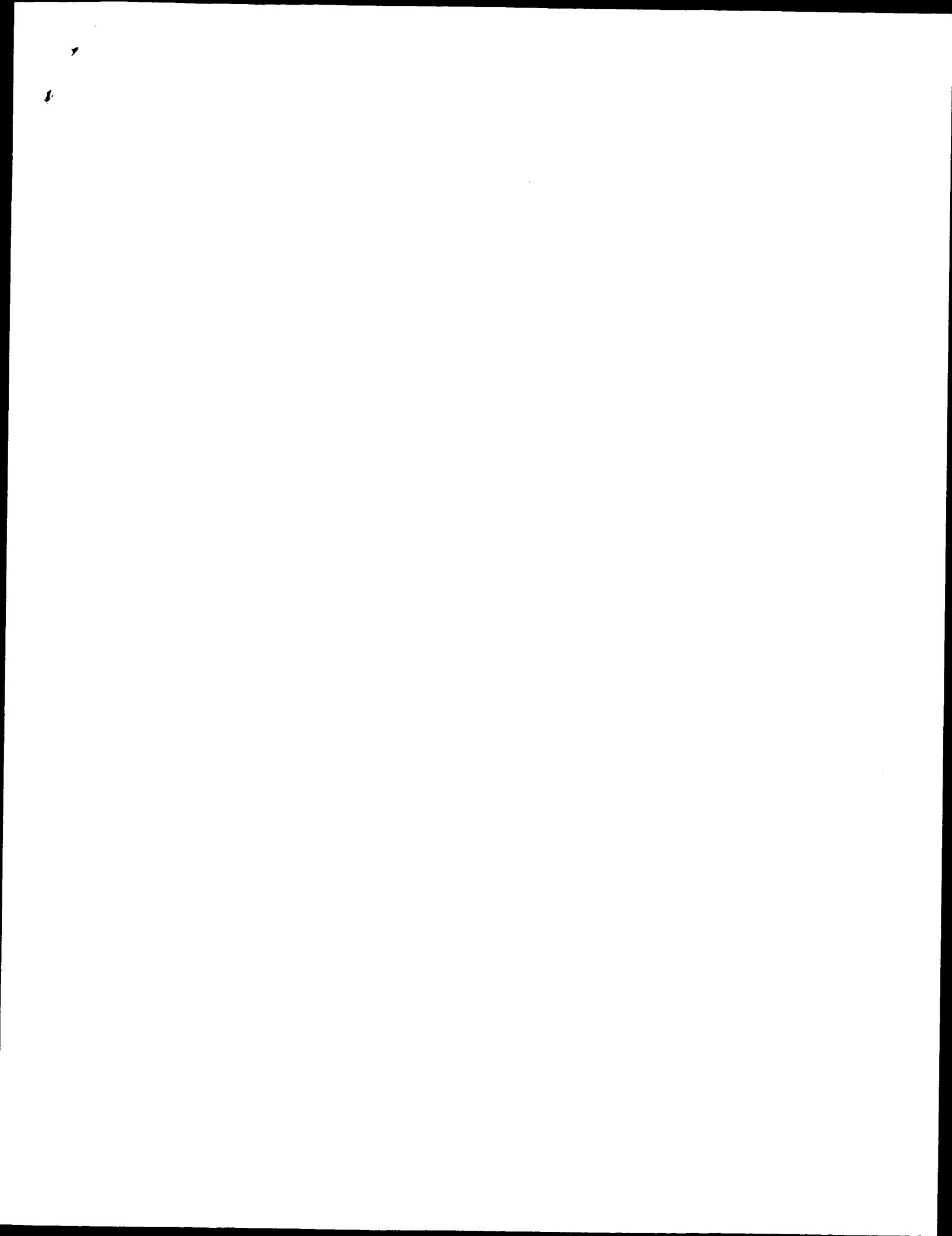
Query Match 7.8%; Score 112.5; DB 4; Length 199;
Best Local Similarity 29.8%; Pred. No. 0.00037; Matches 37; Conservative 16; Mismatches 64; Indels 7; Gaps 4;
Matches 37; Conservative 16; Mismatches 64; Indels 7; Gaps 4;

Qy 3 RLLALVVGALVSSACG-GCVERDSETE-AVYGMTPKILCISCKERSENAETFWRP 59
Db 18 RLLALVGLAATGILTAGVSALLEVYTPKEIFVANGTQKLTC-KPKSTSTRGGLTSVWSF 76

Qy 60 ROKGTEEFVKILRYENEVLOLEEDERFEGRVVWMSRGTKDLSIFTINVTNHSGDY 119
Db 77 QPEGADITVSPPHYSQQVYIGNPPFKDRSW--AGDLDKDASINMNOFHNGTY 133

Qy 120 ECHV 123
Db 134 ICDV 137

Search completed: January 29, 2003, 13:29:59
Job time : 16 Secs



GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: January 29, 2003, 13:28:37 ; Search time: 13 Seconds

(without alignments)
 415.989 Million cell updates/sec

Title: US-09-875-456A-14

Perfect score: 1444

Sequence: 1 MGRLLALVVGALVSSACGG.....QRVVLGLFGIIRCVSRGVV 268

Scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters:

122226

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications A1:*

1: /cgn2_6/podata/1/pubpaa/US08_NEW_PUB.PEP:*

2: /cgn2_6/podata/1/pubpaa/PCT_NEW_PUB.PEP:*

3: /cgn2_6/podata/1/us06_NEW_PUB.COMB.PEP:*

4: /cgn2_6/podata/1/pubpaa/US06_PUB.COMB.PEP:*

5: /cgn2_6/podata/1/pubpaa/US07_NEW_PUB.PEP:*

6: /cgn2_6/podata/1/pubpaa/US07_PUB.COMB.PEP:*

7: /cgn2_6/podata/1/pubpaa/PCTUS_PUB.COMB.PEP:*

8: /cgn2_6/podata/1/pubpaa/US08_PUB.COMB.PEP:*

9: /cgn2_6/podata/1/pubpaa/US09_NEW_PUB.PEP:*

10: /cgn2_6/podata/1/pubpaa/US09_PUB.COMB.PEP:*

11: /cgn2_6/podata/1/pubpaa/US10_NEW_PUB.PEP:*

12: /cgn2_6/podata/1/pubpaa/US10_PUB.COMB.PEP:*

13: /cgn2_6/podata/1/pubpaa/US60_NEW_PUB.PEP:*

14: /cgn2_6/podata/1/pubpaa/US60_PUB.COMB.PEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
 US-09-875-456A-14
 ; Sequence 14 Application US/09875456A
 ; Patent No. US200405229A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Qin, Ning
 ; APPLICANT: Codd, Ellen
 ; APPLICANT: D'Andrea, Michael
 ; TITLE OF INVENTION: DNA encoding human betala sodium channel subunit
 ; FILE REFERENCE: ORT-1221
 ; CURRENT APPLICATION NUMBER: US/09-875-456A
 ; CURRENT FILING DATE: 2001-09-10
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 14
 ; LENGTH: 268
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-875-456A-14

ALIGNMENTS

Query Match 100.0%; Score 1444; DB 10; Length 268;
 Best Local Similarity 100.0%; Pred. No. 2.1e-127;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGRLLALVVGALVSSACGGCTEVDS...TEAVGMTPKILCISCKRASETNAETFWTR	60
Db	1	MGRLLALVVGALVSSACGGCTEVDS...TEAVGMTPKILCISCKRASETNAETFWTR	60
Qy	61	OKGKTEEFVKLRYNEVQELEDEERFGRGVWNGSGTKDODLSPIITNTYNTGDY	120
Db	61	QKGKTEEFVKLRYNEVQELEDEERFGRGVWNGSGTKDODLSPIITNTYNTGDY	120
Qy	121	CHVRLLFENYEINTSVKKHIEWDKGEGAACTFTVTHRAWRDRMVAORTGWL	180
Db	121	CHVRLLFENYEINTSVKKHIEWDKGEGAACTFTVTHRAWRDRMVAORTGWL	180
Qy	181	CAWPANPOORAECEGGSPPCPQLWPFLSSPRRGCGSMPYHRSGCYTOLCHLCMTS	240
Db	181	CAWPANPOORAECEGGSPPCPQLWPFLSSPRRGCGSMPYHRSGCYTOLCHLCMTS	240
Qy	241	GRCLSLSLSRVVLGLPGITIRCVSRGVV	268

Result No.	Score	Query Match Length	DB ID	Description
1	1444	100.0	268	10 US-09-875-456A-14
2	751	52.0	218	10 US-09-957-579-44
3	749	51.9	218	9 US-10-029-191-20
4	258.5	17.9	159	10 US-03-997-579-22
5	258.5	17.9	215	10 US-03-997-579-22
6	257.5	17.8	159	10 US-03-997-579-23
7	257.5	17.8	191	9 US-10-029-191-4
8	257.5	17.8	215	9 US-10-029-191-2
9	257.5	17.8	215	10 US-03-997-579-1
10	25.1	17.4	111	9 US-10-029-191-5
11	114.5	7.9	269	9 US-10-028-172-330
12	110.5	7.7	215	9 US-09-992-598-389
13	110.5	7.7	215	9 US-09-989-193A-389
14	110.5	7.7	215	9 US-09-989-135-389
15	110.5	7.7	215	9 US-09-990-44-389
16	110.5	7.7	215	9 US-09-989-130-389
17	110.5	7.7	215	9 US-09-990-389
18	110.5	7.7	215	9 US-09-991-181-389
19	110.5	7.7	215	9 US-09-993-1687-389

Db 241 GRCLLSLSQRVVLGLPGIIRCVSRGVV 268

RESULT 2

US-09-997-579-44

; Sequence 44; Application US/09997579

; Patent No. US20020113203A1

; GENERAL INFORMATION:

; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodium channel

; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses thereof

; FILE REFERENCE: 674558-2001

; CURRENT APPLICATION NUMBER: US/09/997,579

; CURRENT FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: PCT/EP00/01783

; PRIOR APPLICATION NUMBER: 60,129,473

PRIOR FILING DATE: 2000-02-24

NUMBER OF SEQ ID NOS: 47

SOFTWARE: Patentin version 3.1

SEQ ID NO 44

LENGTH: 218

TYPE: PRT

ORGANISM: Rat

US-09-997-579-44

Query Match Best Local Similarity 52.0%; Score 751; DB 10; Length 218; Matches 144; Conservative 92.9%; Pred. No. 7; Re-63; 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MGRLLLAVGALVSSACGGCVERDSETEAVYGMTPKILCISCKRSSTTAETFTWTR

Db 1 MGRLLLAVGALVSSACGGCVERDSETEAVYGMTPKILCISCKRSSTTAETFTWTR 60

Qy 61 CHVYRLIFFENYERHTSVVKIKHLEWVDKGESGAA 155

Db 121 CHVYRLIFFENYERHTSVVKIKHLEWVDKNAKNDMA 155

RESULT 4

US-09-997-579-22

; Sequence 22; Application US/09997579

; Patent No. US20020113203A1

; GENERAL INFORMATION:

; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodium channel

; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses thereof

; FILE REFERENCE: 674558-2001

; CURRENT APPLICATION NUMBER: US/09/997,579

; CURRENT FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: PCT/EP00/01783

PRIOR FILING DATE: 2000-02-24

NUMBER OF SEQ ID NOS: 47

SOFTWARE: Patentin version 3.1

SEQ ID NO 22

LENGTH: 159

TYPE: PRT

ORGANISM: Homo sapiens

US-09-997-579-22

Query Match Best Local Similarity 43.2%; Score 258.5; DB 10; Length 159; Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 5 LAIVVAGALVSSACGGCVERDSETEAVYGMTPKILCISCKRSSTTAETFTWTRQKGT 64

Db 10 LASIVVAGALVSSACGGCVERDSETEAVYGMTPKILCISCKRSSTTAETFTWTRQKGT 64

Qy 65 EEFVKILRVEVNLQLEDERFEGRVRVNGSGRTKDLQDISIFITVTVNHSQGDYEBCHVY 124

Db 70 KDFL-IYEVNRHQEVESP-FQGR-QWNGS--XLDQDVSIIVNLNSGLYTCNS 123

Qy 125 RLLFFENYERHTSVVKIKHLEWVDK-GB 151

Db 124 RREFEFAHRPFVKTTRLIPRVTTEEAGE 151

RESULT 5

US-09-997-579-2

; Sequence 2; Application US/09997579

; Patent No. US20020113203A1

; GENERAL INFORMATION:

; APPLICANT: Cambridge University Technical Services

; TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodium channel

; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses thereof

; FILE REFERENCE: 674558-2001

; CURRENT APPLICATION NUMBER: US/09/997,579

; CURRENT FILING DATE: 2002-04-05

; PRIOR APPLICATION NUMBER: PCT/EP00/01783

PRIOR FILING DATE: 2000-02-24

NUMBER OF SEQ ID NOS: 47

SOFTWARE: Patentin version 3.1

SEQ ID NO 2

LENGTH: 215

TYPE: PRT

ORGANISM: Lepus Sp.

US-10-029-191-20

Query Match Best Local Similarity 51.9%; Score 749; DB 9; Length 218; Matches 144; Conservative 92.9%; Pred. No. 1.2e-62; 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MGRLLLAVGALVSSACGGCVERDSETEAVYGMTPKILCISCKRSSTTAETFTWTR 60

Db 121 CHVYRLIFFENYERHTSVVKIKHLEWVDKNAKNDMA 155

; ORGANISM: Homo sapiens
; US-09-997-579-2

Query Match 17.9%; Score 258.5; DB 10; Length 215;
Best Local Similarity 43.2%; Pred. No. 7.2e-17;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 5 LALWVGALVSSACGGCWEVDSETEAVYGMTKILCISCKERSETNAETFWTRQKG 64
Db 10 LASLVLIVWNSVCFFPVCEVPSTEAVOGNPMKLRCSMCKREEVEATVVFYRPEGG 69
; ORGANISM: Rattus sp.
; US-10-029-191-4

Query Match 17.9%; Score 258.5; DB 10; Length 215;
Best Local Similarity 43.2%; Pred. No. 7.2e-17;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 65 EETVKILKRYENEVLQEDERERGRVWNGSGTKDQLDISIFTINTYHNSGDYCHV 124
Db 70 KDFL-IYEVNRNGHOEVSP--FQGRQWGS--KDLQDVSIIVNLNDGLYTCNVS 123
; ORGANISM: Rattus sp.
; US-10-029-191-4

Query Match 17.9%; Score 258.5; DB 10; Length 215;
Best Local Similarity 43.2%; Pred. No. 7.2e-17;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 125 RLUFFENYEHTSVVKHIEVVDK-GE 151
Db 124 REFEFAHRPFVKTRLIPRVTEAGE 151
; ORGANISM: Rattus sp.
; US-09-997-579-23

Query Match 17.9%; Score 258.5; DB 10; Length 215;
Best Local Similarity 43.2%; Pred. No. 7.2e-17;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 126 RLUFFENYEHTSVVKHIEVVDK-GE 151
Db 125 RLUFFENYEHTSVVKHIEVVDK-GE 151
; ORGANISM: Rattus sp.
; US-09-997-579-23

Query Match 17.9%; Score 258.5; DB 10; Length 215;
Best Local Similarity 43.2%; Pred. No. 7.2e-17;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 127 RLUFFENYEHTSVVKHIEVVDK-GE 151
Db 126 RLUFFENYEHTSVVKHIEVVDK-GE 151
; ORGANISM: Rattus sp.
; US-09-997-579-23

Query Match 17.9%; Score 258.5; DB 10; Length 215;
Best Local Similarity 43.2%; Pred. No. 7.2e-17;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 128 RLUFFENYEHTSVVKHIEVVDK-GE 151
Db 129 RLUFFENYEHTSVVKHIEVVDK-GE 151
; ORGANISM: Rattus sp.
; US-09-997-579-23

Query Match 17.9%; Score 258.5; DB 10; Length 215;
Best Local Similarity 43.2%; Pred. No. 7.2e-17;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 130 RLUFFENYEHTSVVKHIEVVDK-GE 151
Db 131 RLUFFENYEHTSVVKHIEVVDK-GE 151
; ORGANISM: Rattus sp.
; US-09-997-579-23

Query Match 17.9%; Score 258.5; DB 10; Length 215;
Best Local Similarity 43.2%; Pred. No. 7.2e-17;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 132 RLUFFENYEHTSVVKHIEVVDK-GE 151
Db 133 RLUFFENYEHTSVVKHIEVVDK-GE 151
; ORGANISM: Rattus sp.
; US-09-997-579-23

Query Match 17.9%; Score 258.5; DB 10; Length 215;
Best Local Similarity 43.2%; Pred. No. 7.2e-17;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 134 RLUFFENYEHTSVVKHIEVVDK-GE 151
Db 135 RLUFFENYEHTSVVKHIEVVDK-GE 151
; ORGANISM: Rattus sp.
; US-09-997-579-23

Query Match 17.9%; Score 258.5; DB 10; Length 215;
Best Local Similarity 43.2%; Pred. No. 7.2e-17;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 136 RLUFFENYEHTSVVKHIEVVDK-GE 151
Db 137 RLUFFENYEHTSVVKHIEVVDK-GE 151
; ORGANISM: Rattus sp.
; US-09-997-579-23

Query Match 17.9%; Score 258.5; DB 10; Length 215;
Best Local Similarity 43.2%; Pred. No. 7.2e-17;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 138 RLUFFENYEHTSVVKHIEVVDK-GE 151
Db 139 RLUFFENYEHTSVVKHIEVVDK-GE 151
; ORGANISM: Rattus sp.
; US-09-997-579-23

Query Match 17.9%; Score 258.5; DB 10; Length 215;
Best Local Similarity 43.2%; Pred. No. 7.2e-17;
Matches 64; Conservative 20; Mismatches 57; Indels 7; Gaps 4;

Qy 140 RLUFFENYEHTSVVKHIEVVDK-GE 151
Db 141 RLUFFENYEHTSVVKHIEVVDK-GE 151
; ORGANISM: Rattus sp.
; US-09-997-579-23

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 1
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 3
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 4
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 5
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 6
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 7
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 8
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 9
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 10
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 11
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 12
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 13
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 14
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 15
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 16
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 60/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 17
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Rattus sp.
; US-10-029-191-2

APPLICANT: Cambridge University Technical Services
 TITLE OF INVENTION: A novel family of beta sub-unit proteins from a voltage gated sodium channel
 FILE REFERENCE: 674556-2001
 CURRENT APPLICATION NUMBER: US/09/997,579
 CURRENT FILING DATE: 2002-04-05
 PRIOR APPLICATION NUMBER: PCT/EP00/01783
 PRIOR FILING DATE: 2000-02-24
 NUMBER OF SEQ ID NOS: 47
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 1
 LENGTH: 215
 TYPE: PRT
 ORGANISM: Rat
 US-09-997-579-1

Query Match 17.8%; Score 257.5; DB 10; length 215;
 Best Local Similarity 44.7%; Pred. No. 9e-17; Matches 59; Conservative 19; Mismatches 47; Indels 7; Gaps 4;

Qy 21 CVEVDESETAVYGMFKILCISCKERSETAETTEFTWFRQKGTTEFVKILRVEENIQL 80
 Db 26 CVERVSETEAVQGPMKURCISCKREVEATTVWFRQKGTTEFVKILRVEENIQL 80
 Qy 81 EEDERFEGRVVWNSRGTKDQLDISIFINVVNTNHSGDYECHYRLPFENHENTSVWK 140
 Db 85 ESP -FOGLQWNS -- KDLQDISITVNVTNLDSGLYTNCSREPEFEAIRPFWKTR 139
 Qy 141 KHLIEWVDK-GE 151
 Db 140 LIPPLRVTEAGE 151

RESULT 10
 US-10-028-191-5
 Sequence 5, Application US/10029191
 Patent No. US2003016453A1
 GENERAL INFORMATION:
 APPLICANT: CURTIS, RORY A.J.
 TITLE OF INVENTION: NOVEL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
 FILE REFERENCE: 210147.00X/511
 CURRENT APPLICATION NUMBER: US/10/029,191
 CURRENT FILING DATE: 2001-12-20
 PRIOR APPLICATION NUMBER: 09/569,978
 PRIOR FILING DATE: 2000-05-12
 PRIOR APPLICATION NUMBER: US 60/134,198
 PRIOR FILING DATE: 1999-05-14
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 5
 LENGTH: 111
 TYPE: PRT
 ORGANISM: Rattus sp.
 US-10-029-191-5

Query Match 17.4%; Score 251; DB 9; length 111;
 Best Local Similarity 50.0%; Pred. No. 1.5e-16; Matches 55; Conservative 14; Mismatches 35; Indels 6; Gaps 3;

Qy 21 CVEVDSETEAVYGMFKILCISKKRSETNAFTTFRQKGTTEFVKILRVEENVQL 80
 Db 2 CVVVPSETEAVQCPMKLRCISCKREVEATTVWFRQKGTTEFVKILRVEENQEV 60
 Qy 81 EEDERFEGRVVWNSRGTKDQLDISIFINVVNTNHSGDYECHYRLPFENHENTSVW 130
 Db 61 ESP -FOGLQWNS -- KDLQDISITVNVTNLDSGLYTNCSREPEFE 105

US-10-028-072-530
 Sequence 530, Application US/10028072
 Publication No. US2003004311A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Beresini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audry
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanaabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang
 TITLE OF INVENTION:
 CURRENT APPLICATION NUMBER: US/10/028,072
 FILE REFERENCE:
 CURRENT FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/049911
 PRIOR FILING DATE: 1997-05-18
 PRIOR APPLICATION NUMBER: 60/056974
 PRIOR FILING DATE: 1997-08-26
 PRIOR APPLICATION NUMBER: 60/059113
 PRIOR FILING DATE: 1997-09-17
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 PRIOR FILING DATE: 1997-10-29

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PRIOR FILING DATE: 1998-02-04
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PRIOR APPLICATION NUMBER: 60/084637

PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090538
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07

Query Match 7.9%; Score 114.5; DB 9; Length 269;
Best Local Similarity 30.6%; Pred. No. 0.0027; Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;

Qy	Dy
3 RILLAVGUGAALVSSACG-GCVENTSET--AVUGMTPKLCLCSKRSSETNATETTWTF	59
18 RWMWSVLAAGLGLTAGVSALEYTPKEITFVANGTQKLTCKFKSTSTTGGLTSVSWP	76
Qy 60 ROKGTBEFFKLRLVENEVILQLESDEBFRGRVWVNGSRKTQDLSPIINTVNHSGDY 119	
Db 77 QPEGADTTVSFFHYSQOGVYLGNNPPFKDRISW--AGDLDKKDASINENNQFIHNTY 133	
Qy 120 ECHV 123	
Db 134 ICDV 137	

RESULT 12
 US 09-992-598-389
 Sequence 389, Application US/09992598
 Patent No. US2002016384A1
 GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi J.
 / APPLICANT: Baker, Kevin P.
 / APPLICANT: Borstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan L.
 / APPLICANT: Ferrara, Napoleone
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerritsen, Mary E.
 / APPLICANT: Goddard, Audrey
 / APPLICANT: Godowski, Paul J.
 / APPLICANT: Grimaldi, J. Christopher
 / APPLICANT: Gurney, Austin L.
 / APPLICANT: Kjavian, Ivar J.
 / APPLICANT: Napier, Mary A.
 / APPLICANT: Pan, James
 / APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Watnabe, Colin K.
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William I.
 / APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE OF INVENTION: Acids Encoding the Same
 FILE REFERENCE: P2730PIC20
 CURRENT APPLICATION NUMBER: US/09/992,598
 CURRENT FILING DATE: 2001-11-14
 PRIOR APPLICATION NUMBER: 60/49787
 PRIOR FILING DATE: 1997-05-16
 PRIOR APPLICATION NUMBER: 60/62250
 PRIOR FILING DATE: 1997-10-17
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 / PRIOR FILING DATE: 1998-06-22
 / PRIOR APPLICATION NUMBER: 60/090252
 / PRIOR FILING DATE: 1998-06-22
 / PRIOR APPLICATION NUMBER: 60/090254
 / PRIOR FILING DATE: 1998-06-22
 / PRIOR APPLICATION NUMBER: 60/090349
 / PRIOR FILING DATE: 1998-06-23

	QY	162	--HRRARWDR	170
	Db	175	FOHTRKWAER	186
RESULT 13				
PRIOR APPLICATION NUMBER: 60/090355		US-09-989-293A-39		
PRIOR FILING DATE: 1998-06-23		Sequence 389, Application US/09989293A		
PRIOR APPLICATION NUMBER: 60/090429		; Patent No. US200117164A1		
PRIOR FILING DATE: 1998-06-24		GENERAL INFORMATION:		
PRIOR APPLICATION NUMBER: 60/090431		APPLICANT: Ashkenazi, Avi J.		
PRIOR FILING DATE: 1998-06-24		APPLICANT: Baker, Kevin P.		
PRIOR APPLICATION NUMBER: 60/090472		APPLICANT: Borstein, David		
PRIOR FILING DATE: 1998-06-24		APPLICANT: Desnoyers, Luc		
PRIOR APPLICATION NUMBER: 60/090444		APPLICANT: Eaton, Dan L.		
PRIOR FILING DATE: 1998-06-24		APPLICANT: Ferrara, Napoleone		
PRIOR APPLICATION NUMBER: 60/090445		APPLICANT: Fong, Sherman		
PRIOR FILING DATE: 1998-06-24		APPLICANT: Gerber, Hanspeter		
PRIOR APPLICATION NUMBER: 60/090542		APPLICANT: Gerritsen, Mary E.		
PRIOR FILING DATE: 1998-06-24		APPLICANT: Goddard, Audrey		
PRIOR APPLICATION NUMBER: 60/090535		APPLICANT: Godowski, Paul J.		
PRIOR FILING DATE: 1998-06-24		APPLICANT: Grimaldi, J. Christopher		
PRIOR APPLICATION NUMBER: 60/090540		APPLICANT: Gurney, Austin L.		
PRIOR FILING DATE: 1998-06-24		APPLICANT: Klaavin, Ivar J.		
PRIOR APPLICATION NUMBER: 60/090542		APPLICANT: Napier, Mary A.		
PRIOR FILING DATE: 1998-06-24		APPLICANT: Paauw, James		
PRIOR APPLICATION NUMBER: 60/090557		APPLICANT: Paoni, Nicholas F.		
PRIOR FILING DATE: 1998-06-24		APPLICANT: Roy, Margaret Ann		
PRIOR APPLICATION NUMBER: 60/090676		APPLICANT: Stewart, Timothy A.		
PRIOR FILING DATE: 1998-06-25		APPLICANT: Tumas, Daniel		
PRIOR APPLICATION NUMBER: 60/090678		APPLICANT: Watansabe, Colin K.		
PRIOR FILING DATE: 1998-06-25		APPLICANT: Williams, P. Mickey		
PRIOR APPLICATION NUMBER: 60/090690		APPLICANT: Wood, William T.		
PRIOR FILING DATE: 1998-06-25		TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic		
PRIOR APPLICATION NUMBER: 60/090694		Acids Encoding the Same		
PRIOR FILING DATE: 1998-06-25		FILE REFERENCE: P2730P1C66		
PRIOR APPLICATION NUMBER: 60/090695		CURRENT APPLICATION NUMBER: US/09-989, 293A		
PRIOR FILING DATE: 1998-06-25		CURRENT FILING DATE: 2001-11-20		
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PRIOR FILING DATE: 1998-06-25		PRIOR FILING DATE: 1997-04-16		
PRIOR APPLICATION NUMBER: 60/090862		PRIOR APPLICATION NUMBER: 60/062250		
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PRIOR FILING DATE: 1998-07-02		PRIOR FILING DATE: 1997-11-24		
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Query Match 7.7%; Score 110.5; DB 9; Length 215;		PRIOR FILING DATE: 1998-06-02		
Best Local Similarity 25.0%; Pred. No. 0_0047; Mismatches 78; ::ndels 37; Gaps 9;		PRIOR FILING DATE: 1998-06-02		
Matches 48; Conservative 29; Mismatches 78; ::ndels 37; Gaps 9;		PRIOR FILING DATE: 1998-06-02		
3 RULALVVGAAVSSACCGCVEDSE--TEAVGTMTRKILCTSCSKRUSSETNAETFTWTFR 60		PRIOR FILING DATE: 1998-06-02		
8 RAVLULIGIQLTALMPIAAVEVITSRULEANGTDAKCTFSSAFPGDALTIV-WNFR 66		PRIOR FILING DATE: 1998-06-02		
61 -OKGTERBFVKILRYEVNLEDFEDERPEGRTWNNESRGTDQLQDISIFINTVNTWHSGD 118		PRIOR FILING DATE: 1998-06-02		
67 PLGGGPBQFV--FYHIDPFPQ-PMSGRPKDRVSDGN--PBYDASILWKLQFDDNGT 120		PRIOR FILING DATE: 1998-06-02		
119 YEVCHVRLLFENYEHTSVWKIHTEWPKGE-----SGACPFVFT----- 161		PRIOR FILING DATE: 1998-06-04		
121 YTCQV-----KNPPDVGTVGBIRISVHVTVRFSETHFLALAIGSACALMIVIVVVL 174		PRIOR FILING DATE: 1998-06-04		

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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
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PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
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; PRIOR FILING DATE: 1998-06-23
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; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090431
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; PRIOR APPLICATION NUMBER: 60/090444
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; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 7.7%; Score 110.5; DB 9; Length 215;
Best Local Similarity 25.0%; Pred. No. 0.0047; 78; Indels 37; Gaps 9;
Matches 48; Conservative 29; Mismatches 78; Indels 37; Gaps 9;

Qy	3 RULALVYGAANVSSAGCGCVFUDSE--TEAVYGMFKLTSCKRSETAETPFWTR
Db	8 RAVLVLIGIQLTALMPLIAVBYTSVRLAEVNTGTDARKCTFSSPAPVGDLATV-WNFR
Qy	61 -OKGKFBFVKLRENEVLOEDERFPEGRVWNGSRRGKDKQDLSIFITVNWNHSGD 118
Db	67 PLDGGPROOF-FYFHDPG-PMSGRFKRVSUN--PERVYAS-TIKWTODNGT 120

QY 119 YECRVYRLLFFENYERNTSVVKKHTEVDKCE-----SGIACPFVT----- 161
 Publication No. US20020193299A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 Acid Encoding the Same
 TITLE OF INVENTION: Acids
 FILE REFERENCE: P2730P1C61
 CURRENT APPLICATION NUMBER: US/09/989, 735
 CURRENT FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049987
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 7.7%; Score 110.5; DB 9; Length 215;
Best Local Similarity 25.0%; Pred 0.0047; 78; Mismatches 48; Conservative 29; Matches 37; Gaps 9;

QY 61 -QKGTEERVKILRYENEVLOLEEDERREGRRVNGSRGKTDQLDSLIFTINVNTNSGD 118
Db 67 PLGGGPBQFV--FYYHIDPFO-PMSGRKDRWSWDG----PERYDASILLWKLQFDNGT 120
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

QY 119 YEVCHVYRLUFFENYEHNTSVVKXHIEVVDKGR-----SGAICPFTV----- 161
Db 121 YTCOV-----KNPPDVGVIGBIRLSVWHTVRFSETMFLALAIGSACALMIVIVVWL 174
PRIOR APPLICATION NUMBER: 60/090254
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PRIOR APPLICATION NUMBER: 60/090349
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

QY 175 FOHRKKRKAER 186
Db 175 FOHRKKRKAER 186

RESULT 15
US-09-990-444-389
; Sequence 319, Application US/09990444
; Publication No. US20020133300A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Boststein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hans Peter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurny, Austin L.
; APPLICANT: Kijavim, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/04937
; PRIOR FILING DATE: 1997-06-15
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/08716
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02

Best Local Similarity 25.0%; Pred. No. 0.0047; Matches 48; Conservative 29; Mismatches 78; Indels 37; Gaps 9;

Qy 3 RLLALVVGAAVLSSACGGCVENDSE--TEAVGNTPKALCISCKRRSNTAETTENWFR 60
 Db 8 RAVLVLGIQIATAMPIAAVEIYNSRVLRAVNGDARLKCTFSSFAPYGVDAFLWT-WNFR 66

Qy 61 --QKGPEEFVYLARYENEVTQLEDERFEGRVVNGSGRTKDIQDLSTIFTINYHSGD 118
 Db 67 PLDGGEPEQFY--FYFHIDPQQ-PMSGRFKDRVSIDGN--PERDASILLWKQFDONGT 120

Qy 119 YECHYVRLPFENYHNTSYVKKHIEWDKG-----SGAACCFPTV----- 161
 Db 121 YTCAQV-----KNPPDVDGVIIGEIRLSVWHTVRSEIHFLALAIGSACALMIIIVVWL 174

Qy 162 --HRRARMWDR 170
 Db 175 FQHYRKERWAER 186

Search completed: January 29, 2003, 13:32:48
 Job time : 14 secs

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GenCore version 5.1.3

OM protein - protein search, using sw model

Run on: January 29, 2003, 13:27:17 ; Search time 18 Seconds
 (without alignments)
 1431.335 Million cell updates/sec

Title: US-09-875-456A-14
 Perfect score: 1444
 Sequence: MGRLLALIVVAGLVSACGGG..... QRRVWGLLEGIIIRCVSRGW 268

Scoring table: BLOSUM62
 Gappp 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR 73.*
 1: pir1:*,
 2: pir2:*,
 3: pir3:*,
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Match length	DB ID	Description
1	783	A55734	54.2	218	sodium channel, voltage-gated, beta-1 chain precursor - human.
2	751	A42737	52.0	218	sodium channel, voltage-gated, beta-1 chain precursor - human.
3	749	A32999	51.9	218	sodium channel, voltage-gated, beta-1 chain precursor - human.
4	110.5	A32999	7.7	246	sodium channel, voltage-gated, beta-1 chain precursor - human.
5	110.5	A61087	7.7	249	sodium channel, voltage-gated, beta-1 chain precursor - human.
6	107	JW0053	7.4	369	sodium channel, voltage-gated, beta-1 chain precursor - human.
7	100	MPRT0	6.9	248	sodium channel, voltage-gated, beta-1 chain precursor - human.
8	98.5	JH0252	6.8	248	sodium channel, voltage-gated, beta-1 chain precursor - human.
9	98.5	I38053	6.8	251	sodium channel, voltage-gated, beta-1 chain precursor - human.
10	98	A39754	6.8	361	sodium channel, voltage-gated, beta-1 chain precursor - human.
11	97.5	A54662	6.8	247	sodium channel, voltage-gated, beta-1 chain precursor - human.
12	94	S16444	6.5	358	sodium channel, voltage-gated, beta-1 chain precursor - human.
13	94	A40033	6.5	358	sodium channel, voltage-gated, beta-1 chain precursor - human.
14	94	JQ1400	6.5	360	sodium channel, voltage-gated, beta-1 chain precursor - human.
15	94	S25011	6.5	360	sodium channel, voltage-gated, beta-1 chain precursor - human.
16	93	A29128	6.4	219	sodium channel, voltage-gated, beta-1 chain precursor - human.
17	92.5	A59311	6.4	1099	sodium channel, voltage-gated, beta-1 chain precursor - human.
18	92	T20992	6.4	5175	sodium channel, voltage-gated, beta-1 chain precursor - human.
19	92	T43290	6.4	5198	sodium channel, voltage-gated, beta-1 chain precursor - human.
20	91.5	A38971	6.3	4302	sodium channel, voltage-gated, beta-1 chain precursor - human.
21	89.5	JW0052	6.2	392	sodium channel, voltage-gated, beta-1 chain precursor - human.
22	85.5	T09402	5.9	1327	sodium channel, voltage-gated, beta-1 chain precursor - human.
23	84	T03225	5.8	948	sodium channel, voltage-gated, beta-1 chain precursor - human.
24	83.5	T16948	5.8	978	sodium channel, voltage-gated, beta-1 chain precursor - human.
25	83	S49846	5.7	189	sodium channel, voltage-gated, beta-1 chain precursor - human.
26	82	159116	5.7	188	sodium channel, voltage-gated, beta-1 chain precursor - human.
27	82	T14275	5.7	1120	sodium channel, voltage-gated, beta-1 chain precursor - human.
28	81.5	A36978	5.6	376	sodium channel, voltage-gated, beta-1 chain precursor - human.
29	81.5	A36978	5.6	2	sodium channel, voltage-gated, beta-1 chain precursor - human.

RESULTS

1

Summary

Alignments

Query Match 54.2%; Score 783; DB 2; Length 218;
 Best Local Similarity 96.8%; Pred. No. 5.2e-63;
 Matches 150; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Ov 1 MGRLLALIVVAGLVSACGGG..... QRRVWGLLEGIIIRCVSRGW 268

Db 1 MGRLLALIVVAGLVSACGGG..... QRRVWGLLEGIIIRCVSRGW 268

Ov 61 QKGTEPFKYLRYENVLEEDERFEGRVMWSRGTCQLDLSIFFTNVNTNHSGYE 120

Db 61 QKGTEPFKYLRYENVLEEDERFEGRVMWSRGTCQLDLSIFFTNVNTNHSGYE 120

QY 121 CHYRLLFENYHENTSVVKKHIEVVDKGESGAA 155
 ||||| ||||| ||||| ||||| ||||| |||||
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C;Accession: A42737
 C;Title: Primary structure and functional expression of the beta 1 subunit of the rat br
 Science, L.L.; De Jongh, K.S.; Patton, D.E.; Reber, B.F.; Offord, J.; Charbonneau, H.; Wa
 R, Isom, B.J.; De Jongh, K.S.; Patton, D.E.; Reber, B.F.; Offord, J.; Charbonneau, H.; Wa
 A;Reference number: A42737; MUID:92271207; PMID:1375395
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid; protein
 A;Residues: I-218 <ISO>
 A;Cross-references: GB:M91808; NID:9206864; PIDN:AAA88513.1; PID:9206865
 A;Experimental source: brain; sequence extracted from NCBI backbone (NCBIP:103298)
 C;Keywords: transmembrane protein

Query Match 52.0%; Score 751; DB 2; Length 218;
 Best Local Similarity 92.9%; Pred. No. 4e-60; Matches 144; Conservative 2; MisMatches 9; Indels 0; Gaps 0; C;Status: preliminary
 QY 1 MGJLLALVYGAAVSSAGGCVVNDSETEAVKMFKILCISCKRSETNAETFTWFR 60
 1 MGJLLALVYGAAVSSAGGCVVNDSETEAVKMFKILCISCKRSETNAETFTWFR 60
 Db 61 QKGFEEFKILRNEYEVOLLEDERPEGRVWNGSRGKDLQDLSTIFITNYNHGDYE 120
 61 QKGFEEFKILRNEYEVOLLEDERPEGRVWNGSRGKDLQDLSTIFITNYNHGDYE 120
 QY 121 CHYRLLFENYHENTSVVKKHIEVVDKGESGAA 155
 121 CHYRLLFENYHENTSVVKKHIEVVDKGESGAA 155

A42737
 sodium channel beta 1 subunit - rat

A42737
 C;Species: Rattus norvegicus (Norway rat)

C;Accession: A42737
 C;Title: Primary structure and functional expression of the beta 1 subunit of the rat br
 Science, L.L.; De Jongh, K.S.; Patton, D.E.; Reber, B.F.; Offord, J.; Charbonneau, H.; Wa
 R, Isom, B.J.; De Jongh, K.S.; Patton, D.E.; Reber, B.F.; Offord, J.; Charbonneau, H.; Wa
 A;Reference number: A42737; MUID:92271207; PMID:1375395
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid; protein
 A;Residues: I-218 <ISO>
 A;Cross-references: GB:M91808; NID:9206864; PIDN:AAA88513.1; PID:9206865
 A;Experimental source: brain; sequence extracted from NCBI backbone (NCBIP:103298)
 C;Keywords: transmembrane protein

Query Match 52.0%; Score 751; DB 2; Length 218;
 Best Local Similarity 92.9%; Pred. No. 4e-60; Matches 144; Conservative 2; MisMatches 9; Indels 0; Gaps 0; C;Status: preliminary
 QY 1 MGJLLALVYGAAVSSAGGCVVNDSETEAVKMFKILCISCKRSETNAETFTWFR 60
 1 MGJLLALVYGAAVSSAGGCVVNDSETEAVKMFKILCISCKRSETNAETFTWFR 60
 Db 60 TTSURFRPDNSRISTIHYNGNPYTEKWSQFRGRVWNG---DISKDGSIWIRN 114
 QY 111 VTYNHSGDYCHYRLLFENYHENTSVVKKHIEVVDK 149
 Db 115 LDYDNGTFCFCDV-----KNPPDVVGFISSDVHLTVDK 147

A42737
 sodium channel protein beta chain - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999
 C;Accession: JC4788
 R;Selcher, S.M.; Howe, J.R.
 Gene 170, 285-286, 1996

R;Barbu, M.; Neurosci. Res. 25, 143-151, 1990
 A;Title: Cloning of the cDNA encoding the sodium channel beta1 subunit from rabbit.

A;Reference number: JC4788; MUID:96235151; PMID:8666261
 A;Accession: JC4788
 A;Molecule type: mRNA
 A;Residues: 1-218 <BEL>

A;Cross references: GB:U35382; NID:910103; PIDN:AB1752.1; PID:9101014
 C;Comment: This protein is composed of a large alpha-chain and two small beta-chains and
 C;Comment: This protein is composed of a large alpha-chain and two small beta-chains and
 C;Genetics:
 A;Gene: obetta1
 C;Keywords: glycoprotein; membrane protein; muscle; transmembrane protein

F;151-182/Domain: transmembrane #status predicted <TM>
 F;93,110,114,135/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.9%; Score 749; DB 2; Length 218;
 Best Local Similarity 92.9%; Pred. No. 6e-60; Matches 144; Conservative 2; MisMatches 9; Indels 0; Gaps 0; C;Status: experimental

Query Match 7.7%; Score 110.5; DB 1; Length 249;
 Best Local Similarity 29.8%; Pred. No. 0.021; Matches 39; Conservative 23; MisMatches 50; Indels 19; Gaps 6; C;Status: experimental

QY 1 MGRLALVVGALVSSACGGCVVENDSETEAVYMTFKLICISKCRSETNAETFTWFR 60
 1 MGRLALVVGALVSSACGGCVVENDSETEAVYMTFKLICISKCRSETNAETFTWFR 60
 QY 61 QKGFEEFKILRNEYEVOLLEDERPEGRVWNGSRGKDLQDLSTIFITNYNHGDYE 120

Db 61 QKGFEEFKILRNEYEVOLLEDERPEGRVWNGSRGKDLQDLSTIFITNYNHGDYE 120

A42737
 myelin P0 protein precursor - horn shark

C;Species: Heterodontus francisci (horn shark)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C;Accession: A32999
 R;Saavedra, R.A.; Fors, L.; Abersold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood, J.; Mol. Evol. 29, 149-156, 1989
 A;Title: The myelin proteins of the shark brain are similar to the myelin proteins of the
 A;Reference number: A32999; MUID:90040744; PMID:2478717
 A;Accession: A32999
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-246 <SAA>
 A;Cross-references: GB:X16714; NID:963976; PIDN:CA837865.1; PID:9446744
 C;Superfamily: myelin P0 protein; immunoglobulin homology <IMM>
 F;41-127/Domain: immunoglobulin homology <IMM>

Query Match 7.7%; Score 110.5; DB 1; Length 246;
 Best Local Similarity 30.3%; Pred. No. 0.021; Matches 30; Conservative 13; MisMatches 43; Indels 13; Gaps 3; C;Status: preliminary
 QY 53 TFTEWTFRQGTERPFVKILRNEYEVOLLEDERPEGRVWNGSRGKDL-QDLSTIFITNYNHGDYE 110
 53 TFTEWTFRQGTERPFVKILRNEYEVOLLEDERPEGRVWNGSRGKDL-QDLSTIFITNYNHGDYE 110
 Db 60 TTSURFRPDNSRISTIHYNGNPYTEKWSQFRGRVWNG---DISKDGSIWIRN 114
 QY 111 VTYNHSGDYCHYRLLFENYHENTSVVKKHIEVVDK 149
 Db 115 LDYDNGTFCFCDV-----KNPPDVVGFISSDVHLTVDK 147

A32999
 myelin P0 protein precursor - horn shark

C;Species: Heterodontus francisci (horn shark)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C;Accession: A32999
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 A;Title: The myelin proteins of the shark brain are similar to the myelin proteins of the
 A;Reference number: A32999; MUID:90040744; PMID:2478717
 A;Accession: A32999
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-246 <SAA>
 A;Cross-references: GB:X16714; NID:963976; PIDN:CA837865.1; PID:9446744
 C;Superfamily: myelin P0 protein; immunoglobulin homology <IMM>
 F;41-127/Domain: immunoglobulin homology <IMM>

Query Match 7.7%; Score 110.5; DB 1; Length 246;
 Best Local Similarity 30.3%; Pred. No. 0.021; Matches 30; Conservative 13; MisMatches 43; Indels 13; Gaps 3; C;Status: preliminary
 QY 53 TFTEWTFRQGTERPFVKILRNEYEVOLLEDERPEGRVWNGSRGKDL-QDLSTIFITNYNHGDYE 110
 53 TFTEWTFRQGTERPFVKILRNEYEVOLLEDERPEGRVWNGSRGKDL-QDLSTIFITNYNHGDYE 110
 Db 60 TTSURFRPDNSRISTIHYNGNPYTEKWSQFRGRVWNG---DISKDGSIWIRN 114
 QY 111 VTYNHSGDYCHYRLLFENYHENTSVVKKHIEVVDK 149
 Db 115 LDYDNGTFCFCDV-----KNPPDVVGFISSDVHLTVDK 147

A32999
 myelin P0 protein precursor - horn shark

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 C;Accession: A32999
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 A;Title: The myelin proteins of the shark brain are similar to the myelin proteins of the
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 A;Accession: A32999
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-246 <SAA>
 A;Cross-references: GB:X16714; NID:963976; PIDN:CA837865.1; PID:9446744
 C;Superfamily: myelin P0 protein; immunoglobulin homology <IMM>
 F;41-127/Domain: immunoglobulin homology <IMM>

Query Match 7.7%; Score 110.5; DB 1; Length 246;
 Best Local Similarity 30.3%; Pred. No. 0.021; Matches 30; Conservative 13; MisMatches 43; Indels 13; Gaps 3; C;Status: preliminary
 QY 53 TFTEWTFRQGTERPFVKILRNEYEVOLLEDERPEGRVWNGSRGKDL-QDLSTIFITNYNHGDYE 110
 53 TFTEWTFRQGTERPFVKILRNEYEVOLLEDERPEGRVWNGSRGKDL-QDLSTIFITNYNHGDYE 110
 Db 60 TTSURFRPDNSRISTIHYNGNPYTEKWSQFRGRVWNG---DISKDGSIWIRN 114
 QY 111 VTYNHSGDYCHYRLLFENYHENTSVVKKHIEVVDK 149
 Db 115 LDYDNGTFCFCDV-----KNPPDVVGFISSDVHLTVDK 147

A32999
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 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-246 <SAA>
 A;Cross-references: GB:X16714; NID:963976; PIDN:CA837865.1; PID:9446744
 C;Superfamily: myelin P0 protein; immunoglobulin homology <IMM>
 F;41-127/Domain: immunoglobulin homology <IMM>

Query Match 7.7%; Score 110.5; DB 1; Length 246;
 Best Local Similarity 30.3%; Pred. No. 0.021; Matches 30; Conservative 13; MisMatches 43; Indels 13; Gaps 3; C;Status: preliminary
 QY 53 TFTEWTFRQGTERPFVKILRNEYEVOLLEDERPEGRVWNGSRGKDL-QDLSTIFITNYNHGDYE 110
 53 TFTEWTFRQGTERPFVKILRNEYEVOLLEDERPEGRVWNGSRGKDL-QDLSTIFITNYNHGDYE 110
 Db 60 TTSURFRPDNSRISTIHYNGNPYTEKWSQFRGRVWNG---DISKDGSIWIRN 114
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 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-246 <SAA>
 A;Cross-references: GB:X16714; NID:963976; PIDN:CA837865.1; PID:9446744
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 F;41-127/Domain: immunoglobulin homology <IMM>

Query Match 7.7%; Score 110.5; DB 1; Length 246;
 Best Local Similarity 30.3%; Pred. No. 0.021; Matches 30; Conservative 13; MisMatches 43; Indels 13; Gaps 3; C;Status: preliminary
 QY 53 TFTEWTFRQGTERPFVKILRNEYEVOLLEDERPEGRVWNGSRGKDL-QDLSTIFITNYNHGDYE 110
 53 TFTEWTFRQGTERPFVKILRNEYEVOLLEDERPEGRVWNGSRGKDL-QDLSTIFITNYNHGDYE 110
 Db 60 TTSURFRPDNSRISTIHYNGNPYTEKWSQFRGRVWNG---DISKDGSIWIRN 114
 QY 111 VTYNHSGDYCHYRLLFENYHENTSVVKKHIEVVDK 149
 Db 115 LDYDNGTFCFCDV-----KNPPDVVGFISSDVHLTVDK 147

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 A;Accession: A32999
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-246 <SAA>
 A;Cross-references: GB:X16714; NID:963976; PIDN:CA837865.1; PID:9446744
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 A;Status: preliminary
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 F;41-127/Domain: immunoglobulin homology <IMM>

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 myelin P0 protein precursor - horn shark

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 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-246 <SAA>
 A;Cross-references: GB:X16714; NID:963976; PIDN:CA837865.1; PID:9446744
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 F;41-127/Domain: immunoglobulin homology <IMM>

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 QY 111 VTYNHSGDYCHYRLLFENYHENTSVVKKHIEVVDK 149
 Db 115 LDYDNGTFCFCDV-----KNPPDVVGFISSDVHLTVDK 147

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 A;Reference number: A32999; MUID:90040744; PMID:2478717
 A;Accession: A32999
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-246 <SAA>
 A;Cross-references: GB:X16714; NID:963976; PIDN:CA837865.1; PID:9446744
 C;Superfamily: myelin P0 protein; immunoglobulin homology <IMM>
 F;41-127/Domain: immunoglobulin homology <IMM>

Query Match 7.7%; Score 110.5; DB 1; Length 246;
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 53 TFTEWTFRQGTERPFVKILRNEYEVOLLEDERPEGRVWNGSRGKDL-QDLSTIFITNYNHGDYE 110
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 C;Accession: A32999
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 A;Accession: A32999
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-246 <SAA>
 A;Cross-references: GB:X16714; NID:963976; PIDN:CA837865.1; PID:9446744
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 F;41-127/Domain: immunoglobulin homology <IMM>

Query Match 7.7%; Score 110.5; DB 1; Length 246;
 Best Local Similarity 30.3%; Pred. No. 0.021; Matches 30; Conservative 13; MisMatches 43; Indels 13; Gaps 3; C;Status: preliminary
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 A;Accession: A32999
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-246 <SAA>
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 F;41-127/Domain: immunoglobulin homology <IMM>

Query Match 7.7%; Score 110.5; DB 1; Length 246;
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 53 TFTEWTFRQGTERPFVKILRNEYEVOLLEDERPEGRVWNGSRGKDL-QDLSTIFITNYNHGDYE 110
 Db 60 TTSURFRPDNSRISTIHYNGNPYTEKWSQFRGRVWNG---DISKDGSIWIRN 114
 QY 111 VTYNHSGDYCHYRLLFENYHENTSVVKKHIEVVDK 149
 Db 115 LDYDNGTFCFCDV-----KNPPDVVGFISSDVHLTVDK 147

A32999
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C;Accession: A32999
 R;Saavedra, R.A.; Fors, L.; Abersold, R.H.; Arden, B.; Horvath, S.; Sanders, J.; Hood, J.; Mol. Evol. 29, 149-156, 198

RESULT 6

JW0053 extracellular signal-regulated kinase (EC 2.7.-.-) 2 - common carp

C;Species: *Cyprinus carpio* (common carp)
 C;Accession: JW0053
 R;Hashimoto, H.; Yokoyama, Y.; Matsuo, Y.; Toyohara, H.; Kohno, M.; Sakaguchi, M.
 J. Biochem. 123, 1031-1035, 1998

A;Title: Existence of two isoforms of extracellular signal-regulated kinase in fish.

A;Reference number: JW0052; MUID:98269030; PMID:9603989

A;Accession: JW0053
 A;Molecule type: mRNA

A;Residues: 1-369 <HAS>

C;Comment: This enzyme is the key enzyme in the intracellular signal transduction pathway
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Query Match 7.4%; Score 107; DB 2; Length 369;
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 Db 1 MATPAVASAPAGGSPNPNSPAGAEMTRGQAFDVGPRYNTSYIGBAGYAMCSAYKRDVKV 60

Qy 52 -----ETTEWTFRQKGTEEFVKLRYE-----NEVLOQBEDERPEGRYVWNGSSRGTK 99
 Db 61 AIKKISPFHQTYCQRTREKILLRKHENITIGINDIIRTTIDQMDVIT-----VQ 114

Qy 100 DQDLSPLSFTINYTMHNGDYECH-----VYLLFFENYERTSVWKR-----IHIEV 146
 Db 115 DUMETDILKLUKQQLHSNDHICFLYQILRGKIKYHSANVLRDLIPSNLINTWDKLI 174

Qy 147 VPKGEGSGAACPPTVTHRARRWRDRWQAVDRGWLCAWPANR-----IQQRANGEGGSSPSCP 202
 Db 175 CDFGLARVADP-----DH-----DHTGFLTEBVATRMRAPBIMLNSKGWTKS-- 217

Qy 203 LQIWK-----PLFLSSPRRGOSMPVPHRRSGYRTOQLCHCMCTSG-----RC 243
 Db 218 IDIWNSVGCILAEMLSNRPF-----PKGH-----YLDQNLHILGILGSPSQDLMC 263

Qy 244 LIISLSQR-WVLGLPPIITC 262
 Db 264 IINIKARYVILSLP--LRC 280

RESULT 7

MRT0 myelin P0 protein precursor - rat

C;Species: *Rattus norvegicus* (Norway rat)
 C;Accession: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Feb-1995
 R;Lemke, G.; Lamar, E.; Patterson, J.
 Neuron 1, 71-83, 1988

A;Title: Isolation and analysis of the gene encoding peripheral myelin protein zero.

A;Reference number: JQ0622; MUID:90166482; PMID:2483091

A;Accession: JQ0622
 A;Molecule type: DNA
 A;Residues: 1-248 <LEM>
 R;Lemke, G.; Axel, R.
 Cell 40, 501-508, 1985

A;Title: Isolation and sequence of a cDNA encoding the major structural protein of perip-

A;Reference number: A22822; MUID:85124601; PMID:257885

A;Accession number: 139378; MUID:94154677; PMID:7509228

A;Molecule type: DNA
 A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-248 <RES>

A;Cross-references: GB:124893; NID:944412; PIDN:AA20656_1; PID:gi29405
 R;Kulkens, T.; Bolhuis, P.A.; Wolterman, R.A.; Kemp, S.; te Nijenhuis, S.; Valentijn, L.
 Nature Genet. 5, 35-39, 1993

A;Title: Deletion of the serine 34 codon from the major peripheral myelin protein P0 gene.

A;Reference number: 158118; MUID:9403514; PMID:7693130

A;Accession: 158118
 A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
 A;Residues: 1-62,64-115 <RE2>

A;Cross-references: GB:566705; NID:9437048; PIDN:AAB28708_1; PID:gi437049

A;Experimental source: disease-state mutant

C;Comment: This protein, a small integral membrane glycoprotein, is the most abundant protein in Schwann cells. It is found only in peripheral nervous system Schwann cells.

C;Genetics: A;Gene: GDB:MPZ; CMT1; CMT1B; HMSN1B
A;Cross-references: GDB:1-125266; OMIM:159440
A;Map position: 1q22-1q23
A;Introns: 23/1; 78/3; 150/1; 195/2; 215/3
C;Superfamily: myelin protein, immunoglobulin homology
C;Keywords: glycoprotein; membrane protein; myelin; Schwann cell; structural protein
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-129/Domain: peripheral myelin #status predicted
F;43-129/Domain: immunoglobulin homology <IM>
F;150-127/Disulfide bonds: #status predicted
F;122/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 6.8%; Score 98.5; DB 1; Length 248;
Best Local Similarity 26.4%; Pred. No. 0.25; Mismatches 61; Indels 5; Gaps 3;
Matches 32; Conservative 23; Mismatches 32; Indels 5; Gaps 3;

Qy 4 LILALVYGAALV-SACGGCDEVDSRTEAVYGMFKILCISKCRSETMAETFEWTFRQK 62
Db 13 ILAVLFLFSSLVLSPQAQATIVYTDRVHGAVGSRVTLHCSFWSSRWVSDSIFT-WRYQPE 71

Qy 63 GTEEFVKILRYENVELQLEDEDERFREGRVWNGRGTOKLQLDLISIFITNTVINYNSGDYECH 122
Db 72 GGDRASIFHYAKGKQPYIPIBVGTRKERTQWGPWRK--DGSIVIHLNDYDNGTTCD 128

Qy 123 V 123
Db 129 V 129

RESULT 9
I38053
myelin protein zero - human
C;Species: Homo sapiens (man)
C;Accession: 17-May-1996 #sequence_revision 17-May-1996 #text_change 21-Jan-2000
R;Rautenstrauss, B.; Neils, E.; Grehl, H.; Pfeiffer, R.A.; Van Broeckhoven, C.
Hum. Mol. Genet. 3, 1701-1702, 1994
A;Title: Identification of a de novo insertional mutation in P0 in a patient with a Deje
A;Reference number: I38053; MUID:95136435; PMID:7503050
A;Accession: I38053
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4,'G',6,'A',8-28,'I',30-31,'A',33-46,'D',48,'V',50-331,'F',333-361 <GOT>
A;Cross-references: EMBL:231718; NID:9469516; PIDN:CAA83513.1; PID:9469517
R;Su, Y.; Brooks, D.G.; Li, L.; Lopera, J.J.; Trofatter, J.A.; Ravetch, J.V.; Lebo, R.V.
Proc. Natl. Acad. Sci. U.S.A. 90, 10565-10560, 1993
A;Title: Myelin protein zero gene mutated in Charcot-Marie-tooth type 1B patients.
A;Reference number: A49643; MUID:94068501; PMID:7504284
A;Accession: A49643
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Position: 50-105 <SUL>
A;Experimental source: Peripheral blood
A;Note: sequence extracted from NCBI backbone (NCBIP:139777)
C;Genetics:
A;Gene: GDB:MPZ; CMT1; CMT1
A;Cross-references: GDB:125266; OMIM:159440
A;Map position: 1q22-1q23
C;Superfamily: myelin P0 protein; immunoglobulin homology <IM>
F;43-129/Domain: immunoglobulin homology <IM>

Query Match 6.8%; Score 98; DB 2; Length 361;
Best Local Similarity 20.1%; Pred. No. 0.43; Mismatches 56; Conservative 49; Mismatches 80; Indels 94; Gaps 16; Matches 56; Conservative 49; Mismatches 80; Indels 94; Gaps 16;

Qy 29 EAVYGMFTKILC-----ISCKRSESETNAETFEWTFRQKGTBFVKIL---RYE---- 74
Db 36 EGAYGMVCSAHNINQKVRVAKKUSPFHQTYCORTIRE-----IKLLRFKHENTIGI 89

Qy 75 NEVLOLEBEDPRPEGRVWNGRSRGTOKLQLDLISIFITNTVINYNSGDYECH-VYRLIFFENE 133
Db 90 NDITRAPTIQMWDVII-----VQDMETDLYKLKTOHLSNDHICFLYQDRLGKYI 143

Qy 134 HNTSYVKK-----IHTEVUDKGESGAACTPFTWTHRARWRWQAVDRTGMLC 181
Db 144 HSANVLRDKPSNLNLNTTCDLKICDFGLARVADP---DH-----DHTGFLT 188

Qy 182 AWPNAR---PQQRAEGEGSSPSPCOLW-----PLFLSSPRRGOSMPYPHR 224
Db 189 EYVATRWRWYRAPPEIMLNKGTYKS---IDTWVGCLAEMLSNRBIF-----PGKRI 235

Qy 225 RSGYRTOJCILCCWMSG-----RCUUSLQR-WVLGLP 256
Db 236 --YLDQNLHILGLGSPSOEDLNCINIKARYVILSLP 271

RESULT 11
A54662
myelin P0 protein - mouse
C;Species: Mus musculus (house mouse)
C;Accession: A54662
C;Cross-references: GDB:1-125266; OMIM:159440
C;Map position: 10-Subunit 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
A;Title: DNA sequence, genomic organization, and chromosomal localization of the mouse F
A;Reference number: A54662; MUID:9124320; PMID:1709914
A;Accession: A54662
A;Status: preliminary

A39754
mitogen-activated protein kinase (EC 2.7.1.-) - African clawed frog
N;Alternate names: M phase MAP kinase
C;Species: Xenopus laevis (African clawed frog)
C;Accession: A39754; S16597
R;Posada, J.; Sanghera, J.; Pelech, S.; Aebersold, R.; Cooper, J.A.
Mol. Cell. Biol. 11, 2517-2528, 1991
A;Title: Tyrosine phosphorylation and activation of homologous protein kinases during oocyte maturation
A;Reference number: A39754; MUID:91203872; PMID:1708093
A;Accession: A39754
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-61 <POS>
A;Cross-references: GB:MG0977
R;Gotch, Y.; Moriyama, K.; Matsuda, S.; Okumura, E.; Kishimoto, T.; Kawasaki, H.; Suzuki
EMBO J. 10, 2661-2668, 1991
A;Title: Xenopus M phase MAP kinase: isolation of its cDNA and activation by MPF.
A;Reference number: S16597; MUID:91330892; PMID:1714387
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-4,'G',6,'A',8-28,'I',30-31,'A',33-46,'D',48,'V',50-331,'F',333-361 <GOT>
C;Cross-references: EMBL:X59813; NID:964893; PIDN:CAA42482.1; PID:964894
C;Superfamily: Kinase-related transforming protein; protein kinase homology <KIN>
F;26-316/Domain: protein kinase homology <KIN>
F;34-42/Region: protein kinase ATP-binding motif

A;Molecule type: DNA
A;Residues: 1-247 <YOU>
A;Cross-references: GB:W62427
C;Superfamily: myelin P0 protein; immunoglobulin homology <IMM>
F;43-128/Domain: immunoglobulin homology <IMM>

Query Match 6.8%; Score 97.5; DB 1; Length 247;
Best Local Similarity 27.3%; Pred. No. 0.31; Mismatches 61; Indels 7; Gaps 3;
Matches 33; Conservative 20; Mismatches 61; Indels 7; Gaps 3;

Qy 4 LLLALVYGAALVSSACGGCYEVDSSTEAVYGMTPKILCTSKCRSETNAETFFEWTRP-OK 62
Db 14 LALFLFSSLVLSPALIVVPTRE--IYGAVASQVTLHCFSFWSENVSDDISFTRYQE 70
Qy 63 GTEETVKVIRYENEVQLQLEDERERGRGVWNGSRGKTDQDLSIFINVTNTHSGYEVCH 122
Db 71 GGDRDAISIHFVAKGQPYIDEVGAFKERIOWGDPWRK---DASIVIHNLDYSDNGFTCD 127
Qy 123 V 123
Db 128 V 128

RESULT 12

S16444 mitogen-activated protein kinase (EC 2.7.1.-) - mouse
N;Alternate names: cell division cycle-2-related protein kinase ERK2
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #text_change 18-Jun-1999
C;Accession: S16444; S15015; PN0480
R;Hs: Wu, J.; Rall, T.B.; Sturgill, T.W.; Weber, H.J.
Nucleic Acids Res. 19, 3743, 1991
A;Title: Sequence of pG42/MAP kinase, a serine/threonine kinase regulated by tyrosine phosphorylation sites in pp42/mitogen-activated protein kinase ERK2
A;Reference number: S16444; MUID:91305126; PMID:1649458
A;Molecule type: mRNA
A;Residues: 1-358 <HER>
A;Cross-references: EMBL:X58712; NID:G53001; PIDN:CAA41548.1; PIDN:g53002
A;Note: part of this sequence was confirmed by protein sequencing
R;Payne, D.M.; Rossomando, A.J.; Martino, P.; Erickson, A.K.; Her, J.H.; Shabanowitz, J.
EMBO J. 10, 885-892, 1991
A;Title: Identification of the regulatory phosphorylation sites in pp42/mitogen-activated protein kinase ERK2
A;Reference number: S15015; MUID:9184134; PMID:1849075
A;Accession: S15015
A;Status: preliminary
A;Molecule type: protein
A;Residues: 171-181, 'X', 183-189 <PAV>
R;Bishler, M.A.; Nagotskaya, T.V.; Visser, J.W.M.; Belyavsky, A.V.
Gene 124, 305-306, 1993
A;Title: Novel CD22-related protein kinases produced in murine hematopoietic stem cells.
A;Reference number: PN0479; MUID:93185941; PMID:844355
A;Accession: PN0480
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 145-195 <ERS>
C;Superfamily: kinase-related transforming protein; protein kinase homology <Kin>
C;Keyword: ATP; cell cycle control; phosphoprotein; phosphotransferase; serine/threonine/F-183/Region: protein kinase ATP-binding motif
F-183/Binding site: phosphate (Thr) (covalent) #status experimental
F-185/Binding site: phosphate (Tyr) (covalent) #status experimental

Query Match 6.5%; Score 94; DB 2; Length 358;
Best Local Similarity 20.1%; Pred. No. 0.98; Mismatches 75; Indels 102; Gaps 17;
Matches 57; Conservative 49; Mismatches 75; Indels 102; Gaps 17;

Qy 29 EAVYGMTPKILC-----ISCKRSETNAETFFEWTRPQKTEEVKIL---RVE- 74
Db 31 ECAVGM-----VCSAVPNLNKVRVAKKISPFHQTYCQTLR-----IKILRFRHEN 80
Qy 75 ---NEVQLQEDDERERGRGVWNGSRGKTDQDLSIFINVTNTHSGYEVCH-VYLIF 129
Db 81 IIGINDLDIRATIEQMKDVY-----VQDLMETDLYKLUKTOMLSDNDHICLYQILRG 134
Qy 130 ENYERHTSVVK-----IHIEVDKGESGAGCPFTVTHRARRDQWADRT 177
Db 135 IKYTHSANLHRDKPSNLINTCDLKICDFGLARVADP--DH-----DHT 179
Qy 178 GWLICAMPANR---PQORAEGBGSSPSCPQLQW-----PLFLSSRRGQSM 220
Db 180 GRPLTEVATRMRABRBMINSKGVIK--IDIVSVCILABMSNRPIF-----P 227
Qy 221 VPHRSRGYRTOLCHICCOMTSQ-----RULSISOR-VYLIF 256
Db 228 GHK---YLQDNLHIGLGSPOEDLNCLINIKARNYLSLP 266

RESULT 14

J01400 MAP kinase 1 (EC 2.7.1.-) - human
N;Alternate names: ERK; extracellular signal-regulated kinase 2 (ERK2); mitogen-activated kinase 1
C;Contains: protein kinase (EC 2.7.1.37)
C;Species: Homo sapiens (man)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 11-Jun-1999
C;Accession: J01400; S21426; S23477; S21578
R;Owaki, H.; Makar, R.; Boulton, T.G.; Cobellis, T.; Geppert, T.D.
Biochem. Biophys. Res. Commun. 182, 1416-1422, 1992
A;Title: Extracellular signal-regulated kinases in T cells: characterization of human ER
A;Reference number: J01400; MUID:92171961; PMID:1540184
A;Accession: J01400
A;Molecule type: mRNA

A;Residues: 1-360 <OWA> NID:gi82190; PIDN:AA58459.1; PID:gi82191
 A;Cross-references: GB:M84489; NID:gi82190; PIDN:AA58459.1; PID:gi82191
 A;Experimental source: cell line Jurkat
 R;Gonzalez, P.A.; Radin, D.L.; Rigby, M.R.; Davis, R.J.
 FEB3 Lett. 304, 169-178, 1992
 A;Reference number: S23426; MUID:92316223; PMID:1315925
 A;Accession: S23426
 A;Molecule type: mRNA
 A;Cross-references: EMBL:Z11695; NID:gi23878; PIDN:CA7753.1; PID:gi23879
 A;Accession: S23427
 A;Molecule type: mRNA
 A;Residues: 1-39, 'Q', 92-360 <GON2>
 A;Cross-references: EMBL:Z11694; NID:gi23880; PIDN:CA7752.1; PID:gi23881
 C;Comment: This enzyme is activated by MAP kinase kinase (see PIR:45100 and PIR:46723).
 C;Genetics:
 A;Gene: GIBP; PRKM1; ERK; MAPK1; ERK2
 A;Cross-references: GDB:135677; OMIM:176948
 A;Map position: 22q11.2-22q11.2
 C;Complex: monomer
 A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
 A;Pathway: MAP kinase cascade
 C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
 F;21-39/Domain: protein kinase homology <KIN>
 F;31-39/Region: protein kinase ATP-binding motif
 F;185/Binding site: phosphate (Thr) (covalent) (by MAP kinase kinase) #status predicted
 F;187/Binding site: phosphate (Tyr) (covalent) (by MAP kinase kinase) #status predicted
 Query March 6.5%; Score 94; DB 1; Length 360;
 Best Local Similarity 20.1%; Pred. No. 0.98; Mismatches 75; Indels 102; Gaps 17;
 Matches 57; Conservative 49; MisMatches 75; Indels 102; Gaps 17;
 Query 29 ENVGMMFKILC-----ISCKRSENAETTEWTFPROKGTEEFKIL---RYE- 74
 Db 33 EGRYGM---VCSAYDNVKRVAIKKISPFBHQTVCORTLRE-----IKILRFRHEN 82
 Query 75 ---NEVLOLEEDERPEGRGVWNGSRGTQDQLDISIFINTVNHSGYECHE-VYRLIFF 129
 Db 83 IIGINDITRAHTIEQMDVYI-----VQDLMETDLYKUJKTOHLSNDHICFLYQILRG 136
 Query 130 ENYEHTNSVVK-----THIEVVDKGESGAACPPFTVHRRARWRDRWQAVRT 177
 Db 137 LKYIHSANVHLRDLKSNLANTTCDLKICDFGLARVAP----DH-----DHT 181
 Query 178 GMUCAWANR---POORABEGSSSPSCPLQW-----PLFLSSPRRGQSMP 220
 Db 230 GRKH---YLDQNHILGILGSPSQEDLNCLNKARNYLSSLP 268
 Query 182 GFLTEYYVATRWYRAPEIMLNSSKGYTKS--IDIWSVGCILAEMSNSRPPIF-----P 229
 Db 221 VPHRRCYRTQLCHLCOMTSG-----RCUUSLZER-WVGLP 256
 Job time : 19 secs
 Search completed: January 29, 2003, 13:29:38

C;Keywords: ATP; phosphotransferase
 F;23-313/Domain: protein kinase homology <KIN>
 F;31-39/Region: protein kinase ATP-binding motif

Query Match 6.5%; Score 94; DB 2; Length 360;
 Best Local Similarity 20.1%; Pred. No. 0.98; Mismatches 75; Indels 102; Gaps 17;
 Matches 57; Conservative 49; MisMatches 75; Indels 102; Gaps 17;
 Query 29 BAVYGMTPKILC-----ISCKRSENAETTEWTFPROKGTEEFKIL---RYE- 74
 Db 33 EGRYGM---VCSAYDNVKRVAIKKISPFBHQTVCORTLRE-----IKILRFRHEN 82
 Query 75 ---NEVLOLEEDERPEGRGVWNGSRGTQDQLDISIFINTVNHSGYECHE-VYRLIFF 129
 Db 83 IIGINDITRAHTIEQMDVYI-----VQDLMETDLYKUJKTOHLSNDHICFLYQILRG 136
 Query 130 ENYEHTNSVVK-----THIEVVDKGESGAACPPFTVHRRARWRDRWQAVRT 177
 Db 137 LKYIHSANVHLRDLKSNLANTTCDLKICDFGLARVAP----DH-----DHT 181
 Query 178 GMUCAWANR---POORABEGSSSPSCPLQW-----PLFLSSPRRGQSMP 220
 Db 230 GRKH---YLDQNHILGILGSPSQEDLNCLNKARNYLSSLP 268
 Query 182 GFLTEYYVATRWYRAPEIMLNSSKGYTKS--IDIWSVGCILAEMSNSRPPIF-----P 229
 Db 221 VPHRRCYRTQLCHLCOMTSG-----RCUUSLZER-WVGLP 256
 Job time : 19 secs
 Search completed: January 29, 2003, 13:29:38

RESULT 15

S2011 protein kinase ERK2 (EC 2.7.1.-) - bovine
 N;Alternate names: extracellular signal-regulated kinase
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Jun-1999
 C;Accession: S25011
 R;ELY, C.M.; Cox, M.E.; Her, J.; Parsons, S.J.
 submitted to the EMBL Data Library, July 1992
 A;Description: Cloning and sequencing of ERK2 from a bovine adrenal medulla cDNA library
 A;Reference number: S25011
 A;Accession: S25011
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-360 <ELY>
 A;Cross-references: EMBL:Z14089; NID:gi336; PIDN:CAA78467.1; PID:gi337
 C;Superfamily: kinase-related transforming protein; protein kinase homology

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OM protein - protein search, using BW model

Run on: January 29, 2003, 13:24:27 ; Search time 11 Seconds

(without alignments)

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence: 1 MGRLLALVGAALVSSACGG ORWVILGLPGIIRCVSRGVW 268

Scoring table: BLOSUM62

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Database : SwissProt_40;*

Score: 1444
Perfect Score: US-09-875-456a-14
Sequence: 1 MGRLLALVGAALVSSACGG ORWVILGLPGIIRCVSRGVW 268
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	783	54.2	218	1 CIB1_HUMAN
2	752	52.1	218	1 CIB1_MOUSE
3	751	52.0	218	1 CIB1_RAT
4	749	51.9	218	1 CIB1_RABBIT
5	258.5	17.9	215	1 CTB3_HUMAN
6	114.5	7.9	215	1 EVA1_MOUSE
7	110.5	7.7	215	1 EVA1_HUMAN
8	110.5	7.7	246	1 MYP0_HETR
9	110.5	7.7	249	1 MYP0_CHICK
10	101	7.0	248	1 MYP0_MOUSE
11	100	6.9	248	1 MYP0_RAT
12	98.5	6.8	248	1 MYP0_HUMAN
13	98	6.8	361	1 MKO1_XENLA
14	94	6.5	181	1 BY55_HUMAN
15	94	6.5	1 MKO1_MOUSE	
16	94	6.5	360	1 MKO1_BOVIN
17	94	6.5	360	1 MKO1_HUMAN
18	93	6.4	219	1 MYP0_BOVIN
19	91	6.3	501	1 2325_HUMAN
20	90.5	6.3	4303	1 PKD1_HUMAN
21	81.5	5.6	444	1 SIRPA_HUMAN
22	81.5	5.6	659	1 YRWA_CAEEL
23	81	5.6	355	1 PLK_CHICK
24	81	5.6	672	1 LOX5_RAT
25	81	5.6	1088	1 PGDS_RAT
26	80	5.5	664	1 PDTC3_SHEEP
27	79.5	5.5	1 CTB1_HUMAN	
28	79	5.5	354	1 PLK_RAT
29	78.5	5.4	111	1 LIV6_HUMAN
30	78.5	5.4	352	1 IHBG_MOUSE
31	78	5.4	356	1 PLK_MOUSE
32	78	5.4	356	1 PLK5_MOUSE
33	78	5.4	757	1 RRP1_IALE2
	7.4	5.4	1 RRP1_IALE3	

ALIGNMENTS

RESULT 1	ID	CIB1_HUMAN	STANDARD;	PRT;	218 AA.
[1]	ID	CIB1_HUMAN	STANDARD;	PRT;	218 AA.
[2]	AC	Q07699	(Rel. 34, Created)		
	DT	01-OCT-1996	(Rel. 34, Last sequence update)		
	DT	15-JUN-2002	(Rel. 41, Last annotation update)		
	DE	Sodium channel beta-1 subunit precursor.			
	GN	SCN1B.			
	OS	homo sapiens (Human).			
	OC	Bukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
	OX	NCBI_TaxID:9606;			
	RN				
	RP	SEQUENCE FROM N.A.			
	RC	SEQUENCE-Brain;			
	RX	MEDLINE=93357746; PubMed=83394762;			
	RA	McClatchey A.I., Cannon S.C., Slaggenhaupt S.A., Gusella J.F.;			
	RA	"The cloning and expression of a sodium channel beta-1 subunit cDNA from human brain.";			
	RL	Hum. Mol. Genet. 2:145-179(1993).			
	RN				
	RP	SEQUENCE FROM N.A.			
	RC	TISSUE=Skeletal muscle, and Heart;			
	RX	MEDLINE=94171787; PubMed=812980;			
	RA	Makita N., Bennett P.B. Jr., George A.L. Jr.;			
	RA	"Voltage-gated Na+ channel beta 1 subunit mRNA expressed in adult human skeletal muscle, heart, and brain is encoded by a single gene.";			
	RT	J. Biol. Chem. 269:7571-7578(1994).			
	RL				
	RN				
	RP	SEQUENCE FROM N.A.			
	RC	TISSUE=Placenta;			
	RX	MEDLINE=95154833; PubMed=7851891;			
	RA	Makita N., Sloan-Brown K., Weghuis D.O., Ropers H.H.,			
	RA	"Genomic organization and chromosomal assignment of the human voltage-gated Na+ channel beta 1 subunit gene (SCN1B).";			
	RT	RT Genomics 23:628-634(1994).			
	RN	[4]			
	RP	VARIANT GFP5+ TRP-121.			
	RX	MEDLINE=95361163; PubMed=9697698;			
	RA	Wallace R.H., Wang D.W., Singh R., Scheffer I.E., George A.L. Jr., Phillips R.A., Saar K., Reis A., Johnson E.W., Sutherland G.R., Berkovic S.F., Mulley J.C.;			
	RA	"Febile seizures and generalized epilepsy associated with a mutation in the Na(+)-channel beta-1 subunit gene SCN1B.";			
	RT	Nat. Genet. 19:366-370(1998).			
	RT	"FUNCTION: CRUCIAL IN THE ASSEMBLY, EXPRESSION, AND FUNCTIONAL MODULATION OF THE HETEROHOMOMERIC COMPLEX OF THE SODIUM CHANNEL. THE BETA-1 SUBUNIT CAN MODULATE MULTIPLE ALPHA SUBUNIT ISOFORMS FROM BRAIN, SKELETAL MUSCLE, AND HEART.			
	-1	"SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A PORR-FORMING ALPHA SUBUNIT, BETA-1 AND BETA-2 SUBUNITS. BETA-1 IS NONCOVALENTLY ASSOCIATED WITH ALPHA, WHILE BETA-2 IS COVALENTLY LINKED BY DISULFIDE BONDS.			

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF0047; Ig_1.

DR SMART; SMO0409; Ig_1.

KW Ionic channel; Transmembrane; Ion transport; Voltage-gated channel;

KW Glycoprotein; Signal; Immunoglobulin domain.

FT SIGNAL 1 22 BY SIMILARITY.

FT CHAIN 23 215 SODIUM CHANNEL BETA-3 SUBUNIT.

FT DOMAIN 23 159 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 160 180 POTENTIAL.

FT DOMAIN 181 215 CYTOSOLIC (POTENTIAL).

FT DOMAIN 32 154 Ig-LIKE C2-TYPE DOMAIN.

FT DISULFID 45 120 POTENTIAL.

FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 215 AA; 24702 MW; 70F6C604E8B26662 CRC64;

Query Match 51.9%; Score 749; DB 1; Length 218;

Best Local Similarity 92.9%;保守性 2; Mismatches 9; Indels 0; Gaps 0;

Matches 144; Conservative 2; Mis matches 9; Indels 0; Gaps 0;

QY 1 MGRLLALVYGAALVSSACCGCDEVSETAEAVGWTFKLICSKRSETNAETFTWTFR 60

Db 1 MGRLLALVYGAALVSSACCGCDEVSETAEAVGWTFKLICSKRSETTAFTTFR 60

QY 61 ORGTEEEFKILRYENEVQLQLEDERFGGRWVNGSRGTQKLDLSIFITNVNTNHSGDY 120

Db 61 ORGTEEEFKILRYENEVQLQLEDERFGGRWVNGSRGTQKLDLSIFITNVNTNHSGDY 120

QY 121 CHYRLIPPEVNEHNTSVKKIIEVDKGESAA 155

Db 121 CHYRLIPPEVNEHNTSVKKIIEVDKGESAA 155

RESULT 5

CTB3_HUMAN STANDARD; PRT; 215 AA.

ID CTB3_HUMAN

AC QNY72; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

RT "Beta3: an additional auxiliary subunit of the voltage-sensitive sodium channel beta-3 subunit precursor."

DE SCN3B.

OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;

RN [1] RSEQUENCE FROM N.A.

RC TISSUE=Brain; MEDLINE=20160948; PubMed=1068874; Morgan K., Stevens E.B., Snow B., Cox P., Dixon A.K., Lee K., Pincock R.D., Hughes J., Richardson P.J., Mizuguchi K., Jackson A.P.;

RA "Beta3: an additional auxiliary subunit of the voltage-sensitive sodium channel beta-3 subunit that modulates channel gating with distinct kinetics.", Proc. Natl. Acad. Sci. U.S.A. 97:2308-2313 (2000).

RN [2] RSEQUENCE FROM N.A.

RC TISSUE=Amygdala; MEDLINE=21154917; PubMed=11230166; Wilmann S., Weil B., Wellenreuther R., Gassnerhuber J., Glassl S., Absorge W., Boehler M., Blöcker H., Bauersachs S., Blum H., Laubser J., Duesterhoeft A., Beyer A., Koehrer K., Strack N., Meves H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Postka A.; "Towards a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs.", Genome Res. 11:422-435 (2001).

RL -!- FUNCTION: MODULATES CHANNEL GATING KINETICS.

CC -!- SUBCELLULAR LOCATION: Type I membrane Protein.

CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

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DR EMBL; AU243396; CAB76825; 1; -

DR EMBL; AU136589; CAB66524; 1; -

DR P66907; 1NEU; HASP; P66907; 1NEU; InterPro; IPR003599; Ig.

RESULT 6

EVAL_MOUSE STANDARD; PRT; 215 AA.

ID EVAL_MOUSE

AC 07025;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE Epithelial V-like antigen 1 precursor.

GN EVAL_OR_EVA.

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;

RN [1] RSEQUENCE FROM N.A.

RC STRAIN=RAG-2; TISSUE=Thymus; MEDLINE=98252857; PubMed=9985423; Ruitner M., Teesalu T., Combalte G.G., Grassi F.; Mariani M., Teesalu T., Combalte G.G., Merati B., Ruitner M., Teesalu T., Combalte G.G., Grassi F.; "Epithelial V-like antigen (EVA), a novel member of the immunoglobulin superfamily, expressed in embryonic epithelia with a potential role as homotypic adhesion molecule in thymus histogenesis.", RT homotypic adhesion molecule in thymus histogenesis.",

RT J. Cell Biol. 141:161-1071 (1998).

CC -!- FUNCTION: Mediates homophilic cell-cell adhesion.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).

CC -!- TISSUE SPECIFICITY: Expressed in liver and gut, skin, and testis but not in thymocytes, lymphocytes, macrophage or dendritic cells or cell lines.

CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

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DR	EMBL; AF030454; AAC40128.1; -.	RC	TISSUE=squamous cell carcinoma;
DR	HSSP; P06907; INEU.	RA	Pictas A., Peterren I., Schluens K., Petersen S.;
DR	MGD; MGJ:1299160; Eva.	RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";
DR	InterPro; IPR030506; Ig_MHC.	RL	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.
DR	InterPro; IPR03596; Ig_v.	RN	[4]
DR	Pfam; PF00047; Ig; 1.	RP	SEQUENCE FROM N.A.
DR	SMART; SM00406; IgV; 1.	RC	TISSUE=lung;
KW	Cell adhesion; Immunoglobulin domain; Transmembrane; Glycoprotein;	RA	Strausberg R.;
FT	SIGNAL 1 26 POTENTIAL.	RL	Submitted (PBC-2001) to the EMBL/GenBank/DDBJ databases.
FT	CHAIN 27 215 EPITHELIAL V-LIKE ANTIGEN 1.	CC	-- FUNCTION: Mediates homophilic cell-cell adhesion.
FT	DOMAIN 27 154 EXTRACELLULAR (POTENTIAL).	CC	-- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
FT	TRANSMEM 155 175 POTENTIAL.	CC	-- TISSUE SPECIFICITY: Expressed in thymocytes and stromal
FT	DOMAIN 176 215 CYTOPLASMIC (POTENTIAL).	CC	cells; expression elevated in some T cell leukemia.
FT	DISULFID 40 130 IG-LIKE V-TYPE DOMAIN.	CC	-- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
FT	CARBONYD 39 39 N-LINKED (GLCNAC. .) (POTENTIAL).	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
FT	CARBONYD 118 118 N-LINKED (GLCNAC. .) (POTENTIAL).	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
SQ	SEQUENCE 215 AA; 2416 MW; F6E836797CE9D5 CRC54;	CC	the European Bioinformatics Institute. There are no restrictions on its
Query Match	7.9%; Score 114.5; DB 1; Length 215;	CC	use by non-profit institutions as long as its content is in no way
Best Local Similarity	24.7%; Pred. No. 0.0016; CC	CC	modified and this statement is not removed. Usage by and for commercial/
Matches	49; Conservative 29; Mismatches 83; Indels 37; Gaps 9;	CC	or send an email to license@ibb-sib.ch).
Qy	4 LLLAVVGLAVSSACCGCVCVEV--DSBTEAVYGMTRKILCISKRSRSETNAETFEWTFR 61	DR	DR
Db	9 VLPVLISLQLTALCPTEAVIYTSGALEAVNGTDVRLKCTFFSFPAPGDAILT-V-WNFRP 67	DR	DR
Qy	62 K--GTEBFVKILRYENEVLEEDERFREGGVWMSRGKTKLQDLSIFTINTVNTHNSDY 119	DR	DR
Db	68 RDGGERQFV--FYYHIDDPF-PMSGRKPVWGN--PERVYDS:LIWKQFDNNTY 121	DR	DR
Qy	120 ECHVYRLLFENFEVHEHTSVKKIIEHVVD-----KGESGACIPTVT----- 161	DR	DR
Db	122 TCQV-----KNPPDVGIGTIRLSVWTPSEIYFLAVALGSACALMIIIVVVVLF 175	DR	DR
Qy	162 --HRRARWRDWRQAVDRT 177	DR	DR
Db	176 QHFRKKEWRADAKEGT 193	DR	InterPro; IPR03006; Ig_MHC.
RESULT 7	EVAL_HUMAN STANDARD; PRT; 215 AA.	DR	EMBL; AF275945; AAF87240.1; -.
ID	EVAL_HUMAN STANDARD; PRT; 215 AA.	DR	EMBL; AF275947; AAC23183.1; -.
AC	06087; 15-JUN-2002 (Rel. 41, Created)	DR	EMBL; BC17774; AAH17774.1; -.
DT	15-JUN-2002 (Rel. 41, last sequence update)	DR	HSSP; P06907; INEU.
DT	15-JUN-2002 (Rel. 41, last annotation update)	DR	Smart; SM00406; IgV; 1.
DE	Bipartitional V-like antigen 1 precursor.	DR	MM, 604873; -.
GN	EVAL OR EVA.	DR	InterPro; IPR03596; Ig_v.
OS	Homo sapiens (Human).	DR	Pfam; PF00047; Ig; 1.
OC	Bukeryott; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DR	SMART; SM00406; IgV; 1.
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	DR	InterPro; IPR03596; Ig_v.
NCBI_TaxID	9606; [1]	DR	EMBL; AF275945; AAF87240.1; -.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275947; AAC23183.1; -.
RP	TISSUE=Liver and Spleen;	DR	EMBL; BC17774; AAH17774.1; -.
RP	MEDLINE=9825857; Pubmed=9585423;	DR	HSSP; P06907; INEU.
OC	Guttinger M., Sutti F., Panigada M., Porcellini S., Merati B.,	DR	Smart; SM00406; IgV; 1.
OC	Mariani M., Teissalu T., Concalez G., Grassi F.; Merati B.,	DR	InterPro; IPR03596; Ig_v.
NCBI_TaxID	9606; [1]	DR	EMBL; AF275945; AAF87240.1; -.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275947; AAC23183.1; -.
RC	TISSUE=lung;	DR	EMBL; BC17774; AAH17774.1; -.
RT	"dendritification" of putative target genes involved in LM02-induced	DR	Smart; SM00406; IgV; 1.
RT	leukemogenesis."	DR	InterPro; IPR03596; Ig_v.
RT	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	(3)	DR	EMBL; AF275947; AAC23183.1; -.
RN	SEQUENCE FROM N.A.	DR	EMBL; BC17774; AAH17774.1; -.
RC	TISSUE=Endometrial tumor;	DR	Smart; SM00406; IgV; 1.
RA	Davenport J.W., Neale G.A.M., Goorha R.M.,	DR	InterPro; IPR03596; Ig_v.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; AF275945; AAF87240.1; -.
RT	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275947; AAC23183.1; -.
RL	(3)	DR	EMBL; BC17774; AAH17774.1; -.
RN	SEQUENCE FROM N.A.	DR	Smart; SM00406; IgV; 1.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR03596; Ig_v.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275945; AAF87240.1; -.
RC	TISSUE=lung;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"dendritification" of putative target genes involved in LM02-induced	DR	EMBL; BC17774; AAH17774.1; -.
RT	leukemogenesis."	DR	Smart; SM00406; IgV; 1.
RT	Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	(3)	DR	EMBL; AF275947; AAC23183.1; -.
RN	SEQUENCE FROM N.A.	DR	Smart; SM00406; IgV; 1.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR03596; Ig_v.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275945; AAF87240.1; -.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275947; AAC23183.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; BC17774; AAH17774.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	Smart; SM00406; IgV; 1.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	[4]	DR	Smart; SM00406; IgV; 1.
RN	SEQUENCE FROM N.A.	DR	InterPro; IPR03596; Ig_v.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR03596; Ig_v.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275945; AAF87240.1; -.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275947; AAC23183.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; BC17774; AAH17774.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	Smart; SM00406; IgV; 1.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	[4]	DR	Smart; SM00406; IgV; 1.
RN	SEQUENCE FROM N.A.	DR	InterPro; IPR03596; Ig_v.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR03596; Ig_v.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275945; AAF87240.1; -.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275947; AAC23183.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; BC17774; AAH17774.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	Smart; SM00406; IgV; 1.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	[4]	DR	Smart; SM00406; IgV; 1.
RN	SEQUENCE FROM N.A.	DR	InterPro; IPR03596; Ig_v.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR03596; Ig_v.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275945; AAF87240.1; -.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275947; AAC23183.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; BC17774; AAH17774.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	Smart; SM00406; IgV; 1.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	[4]	DR	Smart; SM00406; IgV; 1.
RN	SEQUENCE FROM N.A.	DR	InterPro; IPR03596; Ig_v.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR03596; Ig_v.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275945; AAF87240.1; -.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275947; AAC23183.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; BC17774; AAH17774.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	Smart; SM00406; IgV; 1.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	[4]	DR	Smart; SM00406; IgV; 1.
RN	SEQUENCE FROM N.A.	DR	InterPro; IPR03596; Ig_v.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR03596; Ig_v.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275945; AAF87240.1; -.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275947; AAC23183.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; BC17774; AAH17774.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	Smart; SM00406; IgV; 1.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	[4]	DR	Smart; SM00406; IgV; 1.
RN	SEQUENCE FROM N.A.	DR	InterPro; IPR03596; Ig_v.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR03596; Ig_v.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275945; AAF87240.1; -.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275947; AAC23183.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; BC17774; AAH17774.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	Smart; SM00406; IgV; 1.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	[4]	DR	Smart; SM00406; IgV; 1.
RN	SEQUENCE FROM N.A.	DR	InterPro; IPR03596; Ig_v.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR03596; Ig_v.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275945; AAF87240.1; -.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275947; AAC23183.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; BC17774; AAH17774.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	Smart; SM00406; IgV; 1.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	[4]	DR	Smart; SM00406; IgV; 1.
RN	SEQUENCE FROM N.A.	DR	InterPro; IPR03596; Ig_v.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR03596; Ig_v.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275945; AAF87240.1; -.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275947; AAC23183.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; BC17774; AAH17774.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	Smart; SM00406; IgV; 1.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	[4]	DR	Smart; SM00406; IgV; 1.
RN	SEQUENCE FROM N.A.	DR	InterPro; IPR03596; Ig_v.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR03596; Ig_v.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275945; AAF87240.1; -.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275947; AAC23183.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; BC17774; AAH17774.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	Smart; SM00406; IgV; 1.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	[4]	DR	Smart; SM00406; IgV; 1.
RN	SEQUENCE FROM N.A.	DR	InterPro; IPR03596; Ig_v.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR03596; Ig_v.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275945; AAF87240.1; -.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275947; AAC23183.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; BC17774; AAH17774.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	Smart; SM00406; IgV; 1.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	[4]	DR	Smart; SM00406; IgV; 1.
RN	SEQUENCE FROM N.A.	DR	InterPro; IPR03596; Ig_v.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR03596; Ig_v.
RN	SEQUENCE FROM N.A.	DR	EMBL; AF275945; AAF87240.1; -.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275947; AAC23183.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; BC17774; AAH17774.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	Smart; SM00406; IgV; 1.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	EMBL; AF275945; AAF87240.1; -.
RL	[4]	DR	Smart; SM00406; IgV; 1.
RN	SEQUENCE FROM N.A.	DR	InterPro; IPR03596; Ig_v.
RC	TISSUE=squamous cell carcinoma;	DR	EMBL; AF275945; AAF87240.1; -.
RT	Pictas A., Peterren I., Schluens K., Petersen S.;	DR	EMBL; AF275947; AAC23183.1; -.
RT	"Human EVAL gene which is downregulated in lung carcinoma cells.";	DR	EMBL; BC17774; AAH17774.1; -.
RT	Submitted (SPP-2000) to the EMBL/GenBank/DDBJ databases.	DR	Smart; SM00406; IgV; 1.
RL	[4]	DR	InterPro; IPR0359

RESULT 12

MYP0_HUMAN STANDARD; PRT; 248 AA.

ID P25189; Q16072; DT 01-MAY-1992 (Rel. 22, Created)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Myelin Po protein precursor (Myelin protein zero) (Myelin peripheral protein) (MPP).

GN MPZ.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [NCBI_TaxID=9606;]

RP SEQUENCE FROM N.A.

RX MEDLINE=92062068; PubMed=1119967;

RX MEDLINE=92062068; PubMed=1119967;

RX MEDLINE=93356807; PubMed=7688964;

RX Hayasaka K., Ohnishi A., Takada G., Fukushima Y., Murai Y.; Biochem. Biophys. Res. Commun. 180:515-518(1991).

RX type 1"; Biophys. Res. Commun. 194:1317-1322(1993).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=94154677; PubMed=7509228;

RX Pham-Dinh D., Fourbil Y., Blanquet F., Mattei M.-G., Roessel N., Latour P., Chazot G., Vandenberge A.; Dautigny A.; "The major peripheral myelin protein zero gene: structure and localization in the cluster of Fc gamma receptor genes on human chromosome 1q21-3-q23."; Hum. Mol. Genet. 2:2051-2054(1993).

RN [4]

RP REVIEW ON CMT-1B VARIANTS.

RX MEDLINE=95282670; PubMed=7762451;

RX Roa B.B., Lupski J.R.;

RT "Molecular genetics of Charcot-Marie-Tooth disease: a new paradigm for the mechanism of inherited disease"; Adv. Hum. Genet. 22:117-152(1994).

RN [5]

RP REVIEW ON CMT-1B VARIANTS.

RX MEDLINE=94302675; PubMed=7518101;

RX Patel P.I., Lupski J.R.;

RT "Charcot-Marie-Tooth disease: a new paradigm for the mechanism of inherited disease"; Trends Genet. 10:128-133(1994).

RN [6]

RP REVIEW ON CMT-1B AND DSS VARIANTS.

RX MEDLINE=9503460; PubMed=9883935;

RX Nelis E., Hautes N., van Broeckhoven C.;

RT "Mutations in the peripheral myelin genes and associated genes in inherited peripheral neuropathies"; Hum. Mutat. 13:11-28(1999).

RN [7]

RP VARIANT CMT-1B MET-30.

RX MEDLINE=94061030; PubMed=7691726;

RX Hayasaka K., Takada G., Ionesescu V.V.; "Mutations of the myelin Po gene in Charcot-Marie-Tooth neuropathy type 1B"; Hum. Mol. Genet. 2:1369-1372(1993).

RN [8]

RP VARIANT CMT-1B CYS-82.

RX MEDLINE=94083341; PubMed=7505151;

RX Hinomori M., Yoshikawa H., Matsui T., Mitsui Y., Takahashi M., Kaido M., Nishimura T., Sawashii Y., Takada G., Hayasaka K.;

RT "New mutation of the myelin Po gene in a pedigree of Charcot-Marie-Tooth neuropathy 1.";

RL Charcot-Marie-Tooth neuropathy 1.

RN Blochim. Mol. Biol. Int. 31:169-173(1993).

RN [9]

RP VARIANT CMT-1B GLU-90 AND GLU-96.

RX MEDLINE=94035113; PubMed=7633129;

RX Hayasaka K., Hirano M., Sato W., Takada G., Uyemura K., Shimizu N., Bird T.D., Comeally R.M., Chance P.F.; "Charcot-Marie-Tooth neuropathy type 1B is associated with mutations of the myelin Po gene.";

RT Nat. Genet. 5:331-34(1993).

RN [10]

RP VARIANT CMT-1B SER-63 DEL.

RX MEDLINE=94035114; PubMed=7633130;

RX Kulkarni T., Bolhuis P.A., Wolterman R.A., Kemp S., Te Nijenhuis S., Valentijn L.J., Hensels G.W., Jennekens F.G., de Visser M.;

RX Hoofendijk J.E., Baas F.; "Deletion of the serine 34 codon from the major peripheral myelin protein Po gene in Charcot-Marie-Tooth disease type 1B.";

RN [11]

RP VARIANT CMT-1B GLU-96.

RX MEDLINE=94063501; PubMed=7504284;

RX Su Y., Brooks D.G., Li L., Lepesq J., Trofatter J.A., Ravetch J.V., Lebo R.V.;

RT "Myelin protein zero gene mutated in Charcot-Marie-Tooth type 1B patients"; Proc. Natl. Acad. Sci. U.S.A. 90:10856-10860(1993).

RN [12]

RP VARIANT DSS CYS-63 AND ARG-167.

RX MEDLINE=94100981; PubMed=7506095;

RX Hayasaka K., Hirano M., Sawaishi Y., Nanao K., Takahashi T., Roa B.B., Lupski J.R.;

RT "De novo mutation of the myelin Po gene in Dejerine-Sottas disease (hereditary motor and sensory neuropathy type III).";

RN [13]

RP VARIANT CMT-1B LEU-78 AND ASN-134.

RX MEDLINE=95080774; PubMed=7527371;

RX Nelis E., Timmerman V., de Jonghe P., Vandenberge A., Pham-Dinh D., Dautigny A., Marcin J.J., van Broeckhoven C.; "Rapid screening of myelin genes in CMT1 patients by SSCP analysis: identification of new mutations and polymorphisms in the Po gene.";

RN [14]

RP VARIANT CMT-1B PHE-63.

RX MEDLINE=96432254; PubMed=8835320;

RX Blanquet-Grossard F., Pham-Dinh D., Dautigny A., Latour P., Bonnebouche C., Corbillon E., Chazot G., Vandenberge A.; "Charcot-Marie-Tooth type 1B neuropathy: third mutation of serine 63 codon in the major peripheral myelin glycoprotein Po gene.";

RN [15]

RP VARIANT CMT-1B LEU-78 AND CYS-101.

RX MEDLINE=9605511; PubMed=7550231;

RX Latour P., Blanquet F., Nelis E., Bonnebouche C., Chapon F., Diraison P., Ollagnon E., Dautigny A., Pham-Dinh D., Chazot G., Bouchrak M., van Broeckhoven C., Vandenberge A.; "Mutations in the myelin protein zero gene associated with Charcot-Marie-Tooth disease type 1B.";

RN [16]

RP VARIANT DSS PHF-64 DEL.

RX MEDLINE=96212920; PubMed=8630052;

RX Ikegami T., Nicholson G., Ikeda H., Ishida A., Johnston H., Wise G., Ouvrier R., Hayasaka K.; "A novel homozygous mutation of the myelin Po gene producing Dejerine-Sottas disease (hereditary motor and sensory neuropathy type III).";

RT Biomed. Biophys. Res. Commun. 222:107-110(1996).

RN [17]

RP VARIANT CMT-1B THR-135 AND SER-137.

RX MEDLINE=96263736; PubMed=8664899;

DR InterPro; IPR002290; Ser-thr_pkinase.
 DR Pfam; PF00069; pkinase_1.
 DR PROSITE; PS00108; Euk_Pkinase; 1.
 DR SMART; SNO220; S_TKc; 1.
 DR PROSITE; PS01351; MAPK_1.
 DR PROSITE; PS50011; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;
 KW Phosphorylation.

FT DOMAIN 2 316 POLY-ALA.
 FT DOMAIN 28 316 PROTEIN KINASE.
 NP BIND 34 42 PROTEIN_KINASE_DOM; 1.
 FT BINDING 57 57 ATP (BY SIMILARITY).
 ACT SITE 152 152 ATP (PROBABLE).
 FT MOD-RES 188 188 BY SIMILARITY.
 MOD-RES 190 190 PHOSPHORYLATION (ACTIVATES THE KINASE).
 FT MUTAGEN 190 190 PHOSPHORYLATION (ACTIVATES THE KINASE).
 FT MUTAGEN 190 190 K-R: INACTIVATION
 I-Y: INACTIVATION.
 FT MUTAGEN 188 188 T->D; NO EFFECT ON TYR PHOSPHORYLATION.
 FT MUTAGEN 190 190 Y->F: AFFECTS THR PHOSPHORYLATION.

FT CONFLICT 5 5 A -> G (IN REF. 2).
 FT CONFLICT 7 7 S -> A (IN REF. 2).
 FT CONFLICT 29 29 T -> I (IN REF. 2).
 FT CONFLICT 32 32 S -> A (IN REF. 2).
 FT CONFLICT 47 47 C -> D (IN REF. 2).
 FT CONFLICT 49 49 I -> V (IN REF. 2).
 SQ SEQUENCE 361 AA; 41292 MW; 663CBDE5E7BC269C CRC64;

Query Match 6.8%; Score 98; DB 1; Length 361;
 Best Local Similarity 20.1%; Pred. No. 0.1;
 Matches 56; Conservative 49; Mismatches 80; Indels 94; Gaps 16;

QY 29 EAVYGMTPKILC-----ISCKRKSETNAETFWTFRQKTEEFVIL---R-YF----- 74
 Db 36 EAYGMWCSAHCNINKRVAKKISPFHQYFCRTIRE-----IKILLRFKHNIIGI 89

QY 75 NEVTLQLEDDERFRGRVYVNGSRGKGKDQLDLSIFITVNTYHSGGYECH-VYRLLFENYE 133
 Db 90 NDITRAFPTEQMDKVYI-----VQDLMETDLYKLKLTQHLSNDHICFYQIRGLKYI 143

Qy 134 HTMVISVKK-----THEEVTDKGESGAACTPTVTHRRARVRDRWQAVRTGWLIC 181
 Db 144 HSNVLRHLDKPSNLNLNTCDLKDGLARVADP---DH----- 188
 FT DISULFID 44 112 DHTGFLT 188

Qy 182 AWFAFNK---PQQRAGEGSSPSCPQLW-----PLFLSSPRRGQNPVPIR 224
 Db 189 EYVATWRYRABIMLNNSKGYIKS-IDIWISVGCLIAEMLSNSRPFR-----PGK- 235

Qy 225 RSGYRTOLCHLCMTSG-----RCHLISLR-VVGLP 256
 Db 236 ---YLDQNLHILGILGSPSQEDLNCTINLKARNYLISLP 271

RESULT 14

BY55_HUMAN STANDARD; PRT; 181 AA.

ID BY55_HUMAN STANDARD; PRT; 181 AA.

AC 095971; 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-JUN-2002 (Rel. 41, Last annotation update)
 DE CD160 antigen precursor (Natural killer cell receptor BY55).
 GN CD160 OR BY55.
 OC Homo sapiens (Human).
 OC Mammalia; Butharia; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606; [1]

RN SEQUENCE FROM N.A.
 RP MEDLINE=9914268; PubMed=9743336;
 RA Anumathan A., Bensusan A., Boumsell L., Christ A.D., Blumberg R.S.,
 RA Voss S.D., Patel A.T., Robertson M.J., Nadler L.M., Freeman G.J.;
 RT "Cloning of BY55, a novel Ig superfamily member expressed on NK cells,"

RT CTL⁺ and intestinal intraepithelial lymphocytes.".;
 RL J. Immunol. 161:2780-2790 (1998).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=99138795; PubMed=9973372;
 RA Agrawal S., Marquet O.J., Freeman G.J., Tawab A., Bouteiller P.L., Roth P., Bolton W., Ogg G., Bounsell L., Bensusan A.;
 RT "Cutting edge: MHC class I triggering by a novel cell surface ligand costimulates proliferation of activated human T cells.";
 RL J. Immunol. 162:1223-1226 (1999).
 CC -!- FUNCTION: Receptor showing broad specificity for both classical and nonclassical MHC class I molecules.
 CC -!- SUBUNIT: Homomultimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- TISSUE SPECIFICITY: Expressed in spleen, peripheral blood, and small intestine. Expression is restricted to functional NK and T cytotoxic lymphocytes.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- DATABASE: NAME=PROW; NOTE=PROW.1-72-73 (2000);
 CC WWW="http://www.ncbi.nlm.nih.gov/prowguide/1660590458_g.htm".
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and the statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF060981; AAC72302.1; -.
 DR MM; 60463; -.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003600; Ig_like.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00410; Ig like; 1.
 DR Receptor; GPI-anchor; Glycoprotein; Signal; Immunoglobulin domain; Antigen.
 FT SIGNAL 1 26 CH160 ANTIGEN.
 FT CHAIN 27 159 REMOVED IN MATURE FORM (POTENTIAL).
 FT PROPEP 160 181 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 37 119 POTENTIAL.
 FT DISULFID 44 112 DISULFID 61 68 N-LINKED (GLCNAC- . .) (POTENTIAL).
 FT CARBOHYD 28 28 N-LINKED (GlcNAc- . .) (POTENTIAL).
 FT LIPID 137 137 GLP-ANCHOR (BY SIMILARITY).
 FT SEQUENCE 159 159 GPI-ANCHOR (BY SIMILARITY).
 SQ SEQUENCE 181 AA; 19810 MW; EF0091AAC747BBB CRC64;

Query Match 6.5%; Score 94; DB 1; Length 181;
 Best Local Similarity 22.6%; Pred. No. 0.11; Mismatches 57; Indels 38; Gaps 7;

QY 6 ALVGAALAVSACGGCGEVDEDTAEVYGMTPKILISCKRKSETNAETFWTFRQK-- 62
 Db 11 ALAILLAIVDQSGGCINITS-SASQEGTRNLICVWHKKKE--AEGFVVFLCKDRSGD 67

QY 63 -GHEEFPKILRVENYVQLEDERERGRVYVNGSRGKGKDQLDLSIF-ITVNTYHSGGYE 120
 Db 68 CSEPETSKQLRKR-----PGIDNGVGEISQMLFTSQVTPLHSGTQ 111

QY 121 C-----HYRLLFENYHN-TSVKKHIE 145
 Db 112 CCARSQSKGIRLQGHFFSILPTETGNVTVGKQRQHLE 150

RESULT 15

MKO1_MOUSE STANDARD; PRT; 358 AA.

ID MKO1_MOUSE STANDARD; PRT; 358 AA.

AC P27703; 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Mitogen-activated protein kinase 1 (EC 2.7.1.-) (Extracellular signal-regulated kinase 2) (ERK-2) (Mitogen-activated protein kinase 2) (MAP kinase 2) (MAPK-2) (P42-MAPK) (ERT1).
 DE MAPK1 OR PDK1 OR ERK2 OR MAPK.
 CC OS Mus musculus (Mouse), and
 CC Rattus norvegicus (Rat).
 CC Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid=10090, 10116;
 CC RN [1] - SEQUENCE FROM N.A.
 CC RC SPECIES=Rat; STRAIN=Sprague-Dawley; TISSUE=Brain;
 CC RX MEDLINE=91235302; PubMed=2032290;
 CC RA Boulton T.G., Nye S.H., Robbins D.J., Ip N.Y., Radziejewska E.,
 CC RA Morganebber S.D., Depino R.A., Panayotatos N., Cobb M.H.,
 CC RA Yancopoulos G.D.;
 CC RT "ERKs: a family of protein-serine/threonine kinases that are activated and tyrosine phosphorylated in response to insulin and NGF";
 CC RL Cell 65:663-675(1991).
 CC RN [2] - SEQUENCE FROM N.A.
 CC RP SPECIES=Mouse; STRAIN=Swiss; TISSUE=Fibroblast;
 CC RX MEDLINE=91305126; PubMed=649458;
 CC RA Her J.-H., Wu J., Rall T.B., Sturgill T.W., Weber N.J.;
 CC RT "Sequence of p42/MAP kinase, a serine/threonine kinase regulated by tyrosine phosphorylation";
 CC RL Nucleic Acids Res. 19:3743-3743(1991).
 CC RN [3] - SEQUENCE OF 151-189 FROM N.A.
 CC RC SPECIES=Mouse; STRAIN=CB6; TISSUE=Bone marrow;
 CC RX MEDLINE=93105941; PubMed=8444355;
 CC RA Erbhler M.A., Nagorsky T.V., Visser J.W.M., Belyavsky A.V.;
 CC RT "Novel CDC2-related protein kinases produced in murine hematopoietic stem cells";
 CC RL Gene 124:305-306(1993).
 CC RN [4] - PHOSPHORYLATION SITES OF THR-183 AND TYR-185, AND PARTIAL SEQUENCE.
 CC RC SPECIES=Mouse; STRAIN=CB6; TISSUE=Bone marrow;
 CC RX MEDLINE=91184134; PubMed=1849075;
 CC RA Payne D.M., Rossomando A.J., Martino P., Erickson A.K., Her J.-H.,
 CC RA Shababovitz J., Hunt D.F., Weber M.J., Sturgill T.W.;
 CC RT "Identification of the regulatory phosphorylation sites in pp42/microgen-activated protein kinase (MAP kinase)";
 CC RL EMBO J. 10:885-892(1991).
 CC RN [5] - X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 CC RC SPECIES=Rat; STRAIN=Sprague-Dawley; TISSUE=Brain;
 CC RX MEDLINE=94150699; PubMed=8107865;
 CC RT "Atomic structure of the MAP kinase ERK2 at 2.3-A resolution";
 CC RL Nature 367:704-710(1994).
 CC RN [6] - X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 CC RC SPECIES=rat;
 CC RX MEDLINE=97442349; PubMed=9298898;
 CC RA Canagarajah B.J., Khokhatchev A., Cobb M.H., Goldsmith E.J.;
 CC RT "Activation mechanism of the MAP kinase ERK2 by dual phosphorylation";
 CC RL Cell 90:859-859(1997).
 CC RN [7] - AUTOPHOSPHORYLATION.
 CC RC SPECIES=rat;
 CC RX MEDLINE=91296777; PubMed=1712480;
 CC RA Seger R., Ahn N.G., Boulton T.G., Yancopoulos G.D., Panayotatos N.,
 CC RA Radziejewska E., Erickson L., Brailioff R.L., Cobb M.H., Krebs E.G.;
 CC RT "Microtubule-associated protein 2 kinases, ERK1 and ERK2, undergo auto phosphorylation on both tyrosine and threonine residues: implications for their mechanism of activation";
 CC RT "Prok. Natl. Acad. Sci. U.S.A. 88:6142-6146(1991);
 CC -!- FUNCTION: PHOSPHORYLATES MICROTUBULE-ASSOCIATED PROTEIN-2 (MAP2).
 CC CC MYELIN BASIC PROTEIN (MBP), AND ELK-1; MAY PROMOTE ENTRY IN THE CELL CYCLE.

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Search completed: January 29, 2003, 13:28:33
Job time : 13 secs

RESULT 2
 ID Q8WWT42 PRELIMINARY; PRT; 185 AA.
 AC Q8WWT42;
 DT 01-MAR-2002 (TREMBrel. 20, Created)
 DT 01-JUN-2002 (TREMBrel. 21, Last annotation update)
 DE Hypothetical 21.5 kDa protein.
 OS Homo sapiens (Human).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=KIDNEY;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: BC021266; AAH21266.1; -.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; ig; 1.
 KW Hypothetical protein.
 SQ 185 AA; 21497 MW; CFB5BB510DC59800 CRC64;
 Query Match 42.9%; Score 620; DB 4; Length 185;
 Best Local Similarity 95.9%; Pred. No. 1.5e-53; Mismatches 0; Indels 5; Gaps 0;
 Matches 117; Conservative 0; Gaps 0; Indels 0; Gaps 0;
 QV 34 MTKILCISCKRSETNAETFWTFWTFQKGTBFVKLRYENEVNLQLEEDERFEGRVVWN 93
 Db 1 MTKILCISCKRSETNAETFWTFWTFQKGTBFVKLRYENEVNLQLEEDERFEGRVVWN 60
 QY 94 GSGTGTQDLSFTINVTYHNGDYCHVYLLPFENYHNTSVVKIHKLEVVDKGESC 153
 Db 61 GSGTGTQDLSFTINVTYHNGDYCHVYLLPFENYHNTSVVKIHKLEVVDKGESC 120
 QY 154 AA; 155
 DB 121 MA; 122

RESULT 3
 ID Q91Z99 PRELIMINARY; PRT; 215 AA.
 AC Q91Z99;
 DT 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-MAY-2002 (TREMBrel. 20, Last annotation update)
 DE Brain and heart sodium channel beta 3 subunit.
 OS Mus musculus (Mouse).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBP1-TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen C., Avery C., Kazen-Gillespie K., Isom L.L.;
 RT "Mouse brain and heart beta 3 sodium channel cDNA,";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY04036; AAL07512.1; -.

RESULT 4
 ID Q9ULR2 PRELIMINARY; PRT; 230 AA.
 AC Q9ULR2;
 DT 01-MAY-2000 (TREMBrel. 13, Created)
 DT 01-MAY-2000 (TREMBrel. 13, Last sequence update)
 DE KIAA1158 protein (Fragment).
 GN KIAA1158.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1] -
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 DR MEDLINE-20039618; PubMed=10574461;
 RA Hirosewa M., Nagase T., Ishikawa K., Kikuno R., Nomura N., Ohara O.,
 RT "Characterization of cDNA clones selected by the GeneMark analysis
 from size-fractionated cDNA libraries from human brain.";
 RL DNA Res. 6:329-336(1999).
 DR EMBL: AB032984; BAA86472.1; -.
 DR HSSP_P05907; INEU.
 DR InterPro: IPR003599; IG_MHC.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF00047; ig; 1.
 DR SMART; SW00409; IG; 1.
 FT NON_TER 1
 SQ SEQUENCE 230 AA; 26357 MW; B06D5155E5F98 CRC64;
 Query Match 17.9%; Score 258.5; DB 4; Length 230;
 Best Local Similarity 43.2%; Pred. No. 1.6e-17; Mismatches 57; Indels 7; Gaps 4;
 Matches 64; Conservative 20; Gaps 0; Indels 0; Gaps 0;
 QV 5 Lalwgaalvvssacggcnevdsateavgygmtfkilciskrsetnaetfwtfqkgt 64
 Db 25 Laslviilywvsvcfppvcuvevseteavognfmkrciscmkreevattvwefvrpegg 84
 QY 65 EEFVKLRYENEVNLQLEEDERFEGRVVWNRCGKTDLOLQDISIFTINVTYHNGDYCHVY 124
 Db 85 KDFL-IYVRNGHQEVSP-PQGRQLQWNS--KDLQDVSIIVNLNDGLYTGNVS 138
 QY 125 RLFFENYHNTSVVKIHKLEVVDKGESC 151
 DB 139 REFEFAHRPFVTRPLRVTEAGE 166

RESULT 5
 ID Q9UK00 PRELIMINARY; PRT; 215 AA.
 AC Q9UK0;

us-09-875-456a-14.rpt

DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Voltage-gated Sodium channel beta-3 subunit (Sodium channel beta 3 subunit).
 DE SCN3B OR SCNB3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=20160948; PubMed=1068874;
 RA Morgan K., Stevens E.B., Shaw B., Cox P., Dixon A.K., Lee K.,
 RA Pinnoch R.D., Hichens J., Richardson P.J., Mizuguchi K., Jackson A.P.;
 RT "beta3: An additional auxiliary subunit of the voltage-sensitive
 sodium channel that modulates channel gating with distinct kinetics.";
 Proc. Natl. Acad. Sci. U.S.A. 97:2308-2313 (2000).
 [2]
 RP STRAINS-SPRAGUE-DAWLEY; TISSUE=DORSAL ROOT GANGLION;
 RC Siles-Santtilago I., Catterall W.A., Scheuer T.;
 RA Qu Y., Curtiss R., Lawson D., Gibride K., Ge P., Di Stefano P.S.,
 RA Silos-Santtilago I., Catterall W.A., Scheuer T.;
 RT "Differential Modulation of Sodium Channel Gating and Persistent
 Sodium Currents by the beta1, beta2, and beta3 subunits";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AU2243395; CAB76338.1; -;
 DR EMBL; AF378093; ANK55415.1; -;
 DR InterPro; IPR003599; Ig; Ig_MHC.
 DR Pfam; PF00047; Ig; Ig.
 DR SMART; SM00409; Ig; Ig.
 KW Ionic channel
 SQ SEQUENCE 215 AA; 24799 MW; 056B498EP5PABF4F CRC64;
 Query Match 17.8%; Score 257.5; DB 11; Length 215;
 Best Local Similarity 44.7%; Pred. No. 1.8e-17; Indels 7; Gaps 4;
 Matches 59; Conservative 19; Mismatches 47;
 QY 21 CYRDVSEFEAVGGMFKLICSKRRSETNAFTPEFTFQKGTEIJKVIRYENHVLQL 80
 DP 26 CYEVSEPEFEAVQGNPMKLCTCSKMRSEVEATVENVYFREGGKPL-IYEYRHQEV 84
 QY 81 EEDERFEGRVVNGNSRGTKDQDLSIFNTNVNHSGYECHVYRLIFFENYEHNTSVVK 140
 Db 85 ESP-FOGLQWNS--KDLQDVSIITVNLNDGSLYTCTCNVSRIPEFEAKRPFWKTR 139
 QY 141 KTHIEVWDK-GE 151
 Db 140 LIPLRVTEAGE 151

RESULT 6

ONYK4 PRELIMINARY; PRT; 209 AA.

QNYK4; PRELIMINARY; PRT; 209 AA.

DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update).
 DE PZlib.
 Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=95009038; PubMed=9792637;
 RA Zhao Z.J., Zhao R.;
 RT "Purification and cloning of PZR, a binding protein and putative
 physiological substrate of tyrosine phosphatase SHP-2.";
 RL J. Biol. Chem. 273:29367-29372 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Xia J., Liu C.-Y., Yu K., Pan Q., Dai H.-P., Tang X.-X.;
 RT "Molecular cloning of myelin protein zero like gene.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Strauberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF087020; AAC72231.1; -;
 DR EMBL; AF055727; AAP00084.1; -;
 DR EMBL; AF092425; AAD5347.1; -;
 DR EMBL; AF055726; AAP00083.1; -;
 DR EMBL; BC007881; AAC07881.1; -;
 DR HSSP; P06907; INEU.
 DR InterPro; IPR0033006; Ig_MHC.
 DR InterPro; IPR0033596; Ig_v.
 DR InterPro; IPR000920; Myelin_Po.
 DR Pfam; PF00047; Ig; Ig.
 DR SMART; SM00409; Ig; Ig.
 DR PRINTS; PR00213; MYELIN0.
 DR SMART; SM00406; IgV; Ig.
 SQ SEQUENCE 209 AA; 22761 MW; 18BC385959C88329 CRC64;

Query Match 7.9%; Score 114.5; DB 4; Length 209;
 Best Local Similarity 30.6%; Pred. No. 0.0028; Indels 7; Gaps 4;
 Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;

QY 3 RLLALVVGALLAVSSACG-GCVCVDESETE--AVVGETMKLICSKRRSETNAFTPEFTF 59
 DR 18 RWLWVSLAAGLULTAGVSALEVTPKPEKFVANQTGKUTC KFKSTTSITGTSITSVWSF 76
 QY 60 ROKGTEEFVILRYTENEVOLQEBERFSGCRVWNGSRGKTDLODLISITNTVNHSGDY 119
 DR 77 QPEGADTTVSSFFHYSQGVYLVGNYPFPKDRISW--AGDLDKKUDASINNIENMOPFIHNGTY 133
 Db 120 ECHV 123
 Qy 120 ECHV 123
 DR 134 ICDV 137

RESULT 7

ID 095297 PRELIMINARY; PRT; 269 AA.

QY 095297; 095297; 01-MAY-1999 (Tremblrel. 10, Created)
 DR 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DR 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DR Protein ZERO related protein (Myelin protein ZERO-like 1).
 DR PZR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

RN [1] SEQUENCE FROM N.A.
 RX MEDLINE=95009038; PubMed=9792637;
 RA Zhao Z.J., Zhao R.;
 RT "Purification and cloning of PZR, a binding protein and putative
 physiological substrate of tyrosine phosphatase SHP-2.";
 RL J. Biol. Chem. 273:29367-29372 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Xia J., Liu C.-Y., Yu K., Pan Q., Dai H.-P., Tang X.-X.;
 RT "Molecular cloning of myelin protein zero like gene.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Strauberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF087020; AAC72231.1; -;
 DR EMBL; AF055727; AAP00084.1; -;
 DR EMBL; AF092425; AAD5347.1; -;
 DR EMBL; AF055726; AAP00083.1; -;
 DR EMBL; BC007881; AAC07881.1; -;
 DR HSSP; P06907; INEU.
 DR InterPro; IPR0033006; Ig_MHC.
 DR InterPro; IPR0033596; Ig_v.
 DR InterPro; IPR000920; Myelin_Po.
 DR Pfam; PF00047; Ig; Ig.
 DR SMART; SM00409; Ig; Ig.
 DR PRINTS; PR00213; MYELIN0.
 DR SMART; SM00406; IgV; Ig.
 SQ SEQUENCE 269 AA; 29082 MW; A1B299041EE59425 CRC64;

Query Match 7.9%; Score 114.5; DB 4; Length 269;
 Best Local Similarity 30.6%; Pred. No. 0.0038; Indels 7; Gaps 4;
 Matches 38; Conservative 15; Mismatches 64; Indels 7; Gaps 4;

QY	3	RLLAVVGAALVSSAACG-GCVERVSETE-AVYVENTFKLICSKRRRBTNAETPTEVF	59
Db	18	RWLMVSLAALGLLTAGVSLEVTPKEFVANGTQKLT_CKFKSITGGITSVWSWP	76
QY	60	ROKGEEFVKILRYENEVLEDEERFEGRVVWNGSRGKFLDLSITITNVYHGDY	119
Db	77	QPEGADTTVSFFHYSQGVYLGNYPFPKURISW--AGDDKKDASINENMQFIHNGTY	133
Qy	120	ECHV 123	
Db	134	ICDV 137	
RESULT 8			
Q9UEL6		PRELIMINARY;	PRT; 183 AA.
ID		Q9UEL6;	
AC			01-MAY-2000 (T-EMBLrel. 13, Created)
DT			01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DR			01-MAY-2001 (T-EMBLrel. 19, Last annotation update)
DE			Hypothetical 20.2 kDa protein (Fragment).
OS			Homo sapiens (Human).
OC			Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI-TAXID			9606;
RN			[1] Q9IWI4
RP			SEQUENCE FROM N.A.
RA			Rhodes S.; Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL			
DR			EMBL; AL035302; CAM22907; 1; -.
DR			HSSP; P06507; INEU.
DR			InterPro; IPR003006; Ig MHC.
DR			IntePro; IPR003596; Ig_V.
DR			InterPro; IPR00920; Myelin_P0.
DR			PFam; PF00047; ig; 1.
DR			PRINTS; PR00213; MYELINPO.
DR			SMART; SM00406; IgV; 1.
KW			Hypothetical protein.
FT			NON_TER
SQ			SEQUENCE 243 AA; 26551 MW; D4E8B8B8D3C005D CRC64;
Query Match 7.5%; Score 109; DB 4; Length 183; Best Local Similarity 30.8%; Pred. No. 0.0083; Matches 28; Conservative 12; Mismatches 47; Indels 4; Gaps 2; SEQUENCE 183 AA; 20230 MW; 571F77B7C514E280 CRC64;			
Qy	33	GMTFKILCISCKRSRSETNAETPTEVFQKGEEFVKILRYENEVLEDEERFEGRVV	92
Db	25	GTOGKUTC-KFKSTTGGITSVWSWFQPEGADTTVSFFHYSQGVYLGNYPFPKURISW	83
Qy	93	NGSRGKFLDLSITITNVYHGDYECHV	123
Db	84	--AGDLKKDASINENMQFIHNGTYICDV	111
RESULT 9			
Q9UEL4		PRELIMINARY;	PRT; 243 AA.
ID		Q9UEL4	
AC		Q9UEL4;	
DT		01-MAY-2000 (T-EMBLrel. 13, Created)	
DT		01-MAY-2000 (T-EMBLrel. 13, Last sequence update)	
DT		01-MAY-2001 (T-EMBLrel. 19, Last annotation update)	
DE		Hypothetical 26.6 kDa protein (Fragment).	
OS		Homo sapiens (Human).	
OC		Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI-TAXID			[1] Q9IWI4
RN			SEQUENCE FROM N.A.
RA			Rhodes S.; Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL			
DR			EMBL; BC015076; AAH15076; 1; -.
DR			MGC; MGI:1289160; Fra.
DR			InterPro; IPR003006; Ig MHC.
DR			InterPro; PR00047; ig; 1.
DR			PRINTS; PR00213; MYELINPO.
DR			SMART; SM00406; IgV; 1.
KW			Hypothetical protein.
FT			SEQUENCE FROM N.A.
SQ			SEQUENCE 215 AA; 24092 MW; F6E5E36787CF79C4 CRC64;
Qy	4	LLAVVGAALVSSAACCGCDEV-DSETEAVVGMFKILCISCKRSRSETNAETPTEVF	61
Db	9	VLPILLSLQTLQALCPTEAVVIYTSGALEAVNGDVRLIKCTFSSFAPVGDALWT-WNRP	67
Qy	62	K-GTEFVKILRYENEVLEDEERFEGRVVWNGSRGKFLDLSITITNVYHGDY	119
Db	68	RDGGREQFV-FYIYMDPFR-PMGRGFKRORVWDGN---PERVDVSIWLKQFDNGTY	121
Qy	120	ECHVYRLLFENYERNTVVKIHLIEVD-----KGESGAACPTVT-----	161
Db	122	TCQV----KNPPDVDFGLVGTIRLSVWHPSEIYFLAVAIGSACALMIVVVVLF	175
Qy	162	-HRRARWMD 169	
Db	176	OHFRKGRWAD 185	
RESULT 11			
Q96MJ0		PRELIMINARY;	PRT; 203 AA.
ID		Q96MJ0	
AC		Q96MJ0;	
DT		01-DEC-2001 (T-EMBLrel. 19, Created)	

DT 01-DEC-2001 (TREMBREL_19, last sequence update)
DR 01-JUN-2002 (TREMBREL_21, Last annotation update)
CDNA FWJ32309 fib, clone PROST2002960, highly similar to human
DE butyrophilin (BTFL) mRNA.
OS Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kuwano J., Chiba Y.,
Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
Sugiyama T., Irie R., Sato H., Wakamatsu A., Ishii S.,
Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
Kimura K., Matsuo K., Nakajima Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Nagami B.,
Suzuki Y., Sogano S., Naganari K., Masuno Y., Negai K., Isogai T.;
RT "NEDO human cDNA sequencing project";
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK056811; BABT1286.1; -.
DR InterPro; IPR013006; IG_MHC.
DR Pfam; PF00047; ig_1.
SQ SQUENCE 203 AA; 22403 MW; 8035D025584E3A47 CRC64;

Query Match 7.1%; Score 103; DB 4; Length 368;
Best Local Similarity 20.4%; Pred. No. 0.038; Gaps 19;
Matches 66; Conservatyve 52; Mismatches 87; Indels 118; Gaps 19;

Qy 5 LALVGAALV--SSACGGEVSET-----EAVGNTFKILC----- 40
Db 1 MAAVAGANAGGSAGGPEMVRCQVFDDVGPRITNLVIGEGAYM---VCSADVNPK 56

Qy 41 --ISCKRKSESETNAETTFTEFRQKGETEVKIL--RVE-----NEVQLFEEDERFEGRV 90
Db 57 VRVAKKISPFEROTYCOTLRE----IKILLRFRHENTIGINDIRAPTEBQMKDVY 110

Qy 91 VWNGSGRTKQDLSIIFTINVTVHSGDYECH--VRLLFENFEHTSVKK----- 141
Db 111 I-----VQDLMDLYKLTQHSDNHCIVLYQIRGLKYIHSANTLHRDLKPSNL 164

Qy 142 ---IHIEVVKDKBRSGAACTPTVHRRARWRDWRQAVDRTGWLCAWPANR---PQORAE 193
Db 165 LNTTCDLKICDFGLARVADP---DH-----DHTGFLTEYVATRWYRAPEIMLN 209

Qy 194 GEASSSPSCQLQW-----PLPLSSPRRGQSMPVPHRSGRYRTOCLLCCWTS 240
Db 210 SKGTYKS--IDINVSQGTLAEMLSNRPIF-----PGKH---YLDQNLHILGILG 253

Qy 241 G-----RCLISLSQR-VVIGLP 256
Db 254 SPSQEDLNCTINLKARNVSLP 276

RESULT 12
Q8IWG6 PRELIMINARY; PRT; 368 AA.
ID Q8IWG6;
AC DT 01-MAR-2002 (TREMBREL_20, Created)
DT 01-MAR-2002 (TREMBREL_20, Last sequence update)
DT 01-JUN-2002 (TREMBREL_21, Last annotation update)
DE Extracellular signal-regulated kinase 2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
NCBI_TaxID=9031;
IPI [1]
RN RP SQUENCE FROM N.A.
RC TSSSE=PINEAL GLAND;
RA Kababara T., Higashii C., Okano T., Fukada Y.,
RT "Cloning of ERK2 expressed in the chicken pineal gland";
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AV033635; AACB56503.1; -.
DR InterPro; IPR000719; Btk kinase.
DR InterPro; IPR03527; MAD_kin.
DR InterPro; IPR02290; Ser_thr_pk kinase.
DR InterPro; IPR01245; Tyr_pk kinase.
DR Pfam; PF00069; pk kinase_I.
DR ProDom; PD000001; Btk kinase; 1.

Query Match 7.0%; Score 101.5; DB 13; Length 202;
Best Local Similarity 23.5%; Pred. No. 0.052; Gaps 4;
Matches 35; Conservatyve 21; Mismatches 68; Indels 25; Gaps 4;

Qy 12 ALVASSACGGEVDSSTEAVY-----GMTPFKILCISCKRSESETNAETFTFWFROK 62
SQ SQUENCE 202 AA; 22322 MW; 92C2900701B6E1E0 CRC64;

Query Match 7.1%; Score 103; DB 13; Length 368;
Best Local Similarity 20.4%; Pred. No. 0.038; Gaps 19;
Matches 66; Conservatyve 52; Mismatches 87; Indels 118; Gaps 19;

Qy 91 VWNGSGRTKQDLSIIFTINVTVHSGDYECH--VRLLFENFEHTSVKK----- 141
Db 111 I-----VQDLMDLYKLTQHSDNHCIVLYQIRGLKYIHSANTLHRDLKPSNL 164

Qy 142 ---IHIEVVKDKBRSGAACTPTVHRRARWRDWRQAVDRTGWLCAWPANR---PQORAE 193
Db 165 LNTTCDLKICDFGLARVADP---DH-----DHTGFLTEYVATRWYRAPEIMLN 209

Qy 194 GEASSSPSCQLQW-----PLPLSSPRRGQSMPVPHRSGRYRTOCLLCCWTS 240
Db 210 SKGTYKS--IDINVSQGTLAEMLSNRPIF-----PGKH---YLDQNLHILGILG 253

Qy 241 G-----RCLISLSQR-VVIGLP 256
Db 254 SPSQEDLNCTINLKARNVSLP 276

RESULT 13
Q91406 PRELIMINARY; PRT; 202 AA.
AC Q91406;
DT 01-Nov-1996 (TREMBREL_01, Created)
DT 01-NOV-1996 (TREMBREL_01, Last sequence update)
DT 01-MAR-2002 (TREMBREL_20, Last annotation update)
DE IPI.
GN IPI.
OS Salmo sp.
OC Bokuryoto; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
NCBI_TaxID=8031;
RN [1]
RP SQUENCE FROM N.A.
RX MEDLINE-95279970; PubMed=7539051;
RA Stratmann A., Jeserich G.;
RT "Molecular cloning and tissue expression of a cDNA encoding IPI-a P0-
like glycoprotein of trout CNS myelin.";
RL J. Neurochem. 64:427-436 (1995).
DR EMBL; S78261; ARB3399.1; -.
DR HSSP; P05907; INEU;
DR InterPro; IPR00306; IG_MHC.
DR InterPro; IPR03596; IG_v.
DR SMART; SW00405; IGv_1.
DR SMART; SW00405; IGv_1.
SQ SQUENCE 202 AA; 22322 MW; 92C2900701B6E1E0 CRC64;

Query Match 7.0%; Score 101.5; DB 13; Length 202;
Best Local Similarity 23.5%; Pred. No. 0.052; Gaps 4;
Matches 35; Conservatyve 21; Mismatches 68; Indels 25; Gaps 4;

Qy 12 ALVASSACGGEVDSSTEAVY-----GMTPFKILCISCKRSESETNAETFTFWFROK 62
SQ SQUENCE 368 AA; 41942 MW; AGF3A3D27C6C9A44 CRC64;

Query Match 7.1%; Score 103; DB 13; Length 368;
Best Local Similarity 20.4%; Pred. No. 0.038; Gaps 19;
Matches 66; Conservatyve 52; Mismatches 87; Indels 118; Gaps 19;

Qy 5 LALVGAALV--SSACGGEVSET-----EAVGNTFKILC----- 40
Db 1 MAAVAGANAGGSAGGPEMVRCQVFDDVGPRITNLVIGEGAYM---VCSADVNPK 56

Qy 41 --ISCKRKSESETNAETTFTEFRQKGETEVKIL--RVE-----NEVQLFEEDERFEGRV 90
Db 57 VRVAKKISPFEROTYCOTLRE----IKILLRFRHENTIGINDIRAPTEBQMKDVY 110

Qy 91 VWNGSGRTKQDLSIIFTINVTVHSGDYECH--VRLLFENFEHTSVKK----- 141
Db 111 I-----VQDLMDLYKLTQHSDNHCIVLYQIRGLKYIHSANTLHRDLKPSNL 164

Qy 142 ---IHIEVVKDKBRSGAACTPTVHRRARWRDWRQAVDRTGWLCAWPANR---PQORAE 193
Db 165 LNTTCDLKICDFGLARVADP---DH-----DHTGFLTEYVATRWYRAPEIMLN 209

Qy 194 GEASSSPSCQLQW-----PLPLSSPRRGQSMPVPHRSGRYRTOCLLCCWTS 240
Db 210 SKGTYKS--IDINVSQGTLAEMLSNRPIF-----PGKH---YLDQNLHILGILG 253

Qy 241 G-----RCLISLSQR-VVIGLP 256
Db 254 SPSQEDLNCTINLKARNVSLP 276

